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(54) Title: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE (57) Abstract Compounds and methods for treating prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. Vaccines and pharmaceutical compositions for immunotherapy of prostate cancer comprising such polypeptides, or DNA molecules encoding such polypeptides, are also provided, together with DNA molecules for preparing the inventive polypeptides.		

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COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE

TECHNICAL FIELD

The present invention relates generally to compositions and methods for the treatment of prostate cancer. The invention is more particularly related to polypeptides comprising at least a portion of a prostate protein and to DNA molecules encoding such polypeptides. Such polypeptides may be used in vaccines and pharmaceutical compositions for treatment of prostate cancer.

BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

Accordingly, there remains a need in the art for improved vaccines and treatment methods for prostate cancer.

SUMMARY OF THE INVENTION

The present invention provides compounds and methods for immunotherapy of prostate cancer. In one aspect, polypeptides are provided comprising at least an immunogenic portion of a prostate tumor protein or a variant of said protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences and variants thereof.

In related aspects, DNA molecules encoding the above polypeptides are provided. In specific embodiments, such DNA molecules include sequences provided in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220 and 222-224. The present invention further provides expression vectors comprising the above DNA molecules and host cells transformed or transfected with such expression vectors. In preferred embodiments, the host cells are selected from the group consisting of *E. coli*, yeast and mammalian cells.

In another aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, an inventive polypeptide and a known prostate antigen.

The present invention also provides pharmaceutical compositions comprising one or more of the above polypeptides, or a DNA molecule encoding such polypeptides, and a physiologically acceptable carrier, together with vaccines comprising one or more of such polypeptide or DNA molecules in combination with a non-specific immune response enhancer.

In related aspects, pharmaceutical compositions for the treatment of prostate cancer comprising one or more polypeptides and a physiologically acceptable carrier are provided, wherein the polypeptide comprises an immunogenic portion of a prostate tumor protein or of a variant of said protein that differs only in conservative substitutions and/or modifications, the prostate tumor protein being encoded by a DNA molecule having a

sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106 and 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants thereof. The invention also provides vaccines for the treatment of prostate cancer comprising such polypeptides in combination with a non-specific immune response enhancer, together with pharmaceutical compositions and vaccines comprising one or more DNA molecules having a sequence provided in SEQ ID NO: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106 and 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219 and 221. Pharmaceutical compositions and vaccines comprising one or more of the above fusion proteins are also provided.

In yet another aspect, methods are provided for inhibiting the development of prostate cancer in a patient, comprising administering an effective amount of at least one of the above pharmaceutical compositions and/or vaccines.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the immunotherapy of prostate cancer. The inventive compositions are generally polypeptides that comprise at least a portion of a prostate tumor protein. Also included within the present invention are molecules (such as an antibody or fragment thereof) that bind to the inventive polypeptides. Such molecules are referred to herein as "binding agents."

In particular, the subject invention discloses polypeptides comprising at least a portion of a human prostate tumor protein, or a variant of such a protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein includes an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-

65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 181, 188, 191, 193, 194, 198, 203, 204, and 207-224, the complements of said nucleotide sequences and variants thereof. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising a portion of one of the above prostate proteins may consist entirely of the portion, or the portion may be present within a larger polypeptide that contains additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may be immunoreactive and/or antigenic.

As used herein, an "immunogenic portion" of a human prostate tumor protein is a portion that is capable of eliciting an immune response in a patient inflicted with prostate cancer and as such binds to antibodies present within sera from a prostate cancer patient. Immunogenic portions of the proteins described herein may thus be identified in antibody binding assays. Such assays may generally be performed using any of a variety of means known to those of ordinary skill in the art, as described, for example, in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1988. For example, a polypeptide may be immobilized on a solid support (as described below) and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A. Alternatively, a polypeptide may be used to generate monoclonal and polyclonal antibodies for use in detection of the polypeptide in blood or other fluids of prostate cancer patients.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For prostate tumor polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of

one of the above polypeptides, and evaluating the immunoreactivity of the modified polypeptide. For prostate tumor polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to generate antibodies that detect the presence or absence of prostate cancer. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydrophobic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recited nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers

to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

"Polypeptides" as used herein also include combination, or fusion, polypeptides. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic prostate tumor-specific sequences, which are joined via a peptide linkage into a single amino acid chain. The sequences may be joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linked sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

The prostate tumor proteins of the present invention, and DNA molecules encoding such proteins, may be isolated from prostate tumor tissue using any of a variety of methods well known in the art. DNA sequences corresponding to a gene (of a portion thereof) encoding one of the inventive prostate tumor proteins may be isolated from a prostate tumor cDNA library using a subtraction technique as described in detail below. Examples of such DNA sequences are provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Partial DNA sequences thus obtained may be used to design oligonucleotide primers for the amplification of full-length DNA sequences in a polymerase chain reaction (PCR), using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989). Once a DNA sequence encoding a polypeptide is obtained, any of the above modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983).

The prostate tumor polypeptides disclosed herein may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a

growing amino acid chain (see, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963). Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Alternatively, any of the above polypeptides may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the protein in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as CHO cells. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form (*i.e.*, the polypeptides are homogenous as determined by amino acid composition and primary sequence analysis). Preferably, the polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. In certain preferred embodiments, described in more detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods disclosed herein.

In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known prostate antigen, together with variants of such fusion proteins. The fusion proteins of the present invention may also include a linker peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end

of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons require to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Polypeptides of the present invention that comprise an immunogenic portion of a prostate tumor protein may generally be used for immunotherapy of prostate cancer, wherein the polypeptide stimulates the patient's own immune response to prostate tumor cells. In further aspects, the present invention provides methods for using one or more of the

immunoreactive polypeptides encoded by a DNA molecule having a sequence provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224 (or fusion proteins comprising one or more such polypeptides and/or DNA encoding such polypeptides) for immunotherapy of prostate cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease. Accordingly, the above immunoreactive polypeptides (or fusion proteins or DNA molecules encoding such polypeptides) may be used to treat prostate cancer or to inhibit the development of prostate cancer. The polypeptides may be administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs.

In these aspects, the polypeptide or fusion protein is generally present within a pharmaceutical composition and/or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. The vaccines may comprise one or more of such polypeptides and a non-specific immune response enhancer, such as an adjuvant, biodegradable microsphere (*e.g.*, polylactic galactide) or a liposome (into which the polypeptide is incorporated). Pharmaceutical compositions and vaccines may also contain other epitopes of prostate tumor antigens, either incorporated into a combination polypeptide (*i.e.*, a single polypeptide that contains multiple epitopes) or present within a separate polypeptide.

Alternatively, a pharmaceutical composition or vaccine may contain DNA encoding one or more of the above polypeptides, such that the polypeptide is generated *in situ*. In such pharmaceutical compositions and vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an epitope of a prostate cell antigen on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*, vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the

use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al., *PNAS* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in published PCT application WO 90/11092, and Ulmer et al., *Science* 259:1745-1749, 1993, reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunotherapy of other diseases. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Between 1 and 10 doses may be administered over a 3-24 week period. Preferably, 4 doses are administered, at an interval of 3 months, and booster administrations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that is effective to raise an immune response (cellular and/or humoral) against prostate tumor cells in a treated patient. A suitable immune response is at least 10-50% above the basal (*i.e.*, untreated) level. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 μ g. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.01 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary

depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax and/or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and/or magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactic glycolide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of immune response, such as lipid A, *Bordella pertussis* or *Mycobacterium tuberculosis*. Such adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ).

Polypeptides disclosed herein may also be employed in *ex vivo* treatment of prostate cancer. For example, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as CellPro Incorporated's (Bothell, WA) CEPRATE™ system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

Polypeptides of the present invention may also, or alternatively, be used to generate binding agents, such as antibodies or fragments thereof, that are capable of detecting metastatic human prostate tumors. Binding agents of the present invention may generally be prepared using methods known to those of ordinary skill in the art, including the representative procedures described herein. Binding agents are capable of differentiating between patients with and without prostate cancer, using the representative assays described

herein. In other words, antibodies or other binding agents raised against a prostate tumor protein, or a suitable portion thereof, will generate a signal indicating the presence of primary or metastatic prostate cancer in at least about 20% of patients afflicted with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without primary or metastatic prostate cancer. Suitable portions of such prostate tumor proteins are portions that are able to generate a binding agent that indicates the presence of primary or metastatic prostate cancer in substantially all (*i.e.*, at least about 80%, and preferably at least about 90%) of the patients for which prostate cancer would be indicated using the full length protein, and that indicate the absence of prostate cancer in substantially all of those samples that would be negative when tested with full length protein. The representative assays described below, such as the two-antibody sandwich assay, may generally be employed for evaluating the ability of a binding agent to detect metastatic human prostate tumors.

The ability of a polypeptide prepared as described herein to generate antibodies capable of detecting primary or metastatic human prostate tumors may generally be evaluated by raising one or more antibodies against the polypeptide (using, for example, a representative method described herein) and determining the ability of such antibodies to detect such tumors in patients. This determination may be made by assaying biological samples from patients with and without primary or metastatic prostate cancer for the presence of a polypeptide that binds to the generated antibodies. Such test assays may be performed, for example, using a representative procedure described below. Polypeptides that generate antibodies capable of detecting at least 20% of primary or metastatic prostate tumors by such procedures are considered to be useful in assays for detecting primary or metastatic human prostate tumors. Polypeptide specific antibodies may be used alone or in combination to improve sensitivity.

Polypeptides capable of detecting primary or metastatic human prostate tumors may be used as markers for diagnosing prostate cancer or for monitoring disease progression in patients. In one embodiment, prostate cancer in a patient may be diagnosed by evaluating a biological sample obtained from the patient for the level of one or more of the

above polypeptides, relative to a predetermined cut-off value. As used herein, suitable "biological samples" include blood, sera, urine and/or prostate secretions.

The level of one or more of the above polypeptides may be evaluated using any binding agent specific for the polypeptide(s). A "binding agent," in the context of this invention, is any agent (such as a compound or a cell) that binds to a polypeptide as described above. As used herein, "binding" refers to a noncovalent association between two separate molecules (each of which may be free (*i.e.*, in solution) or present on the surface of a cell or a solid support), such that a "complex" is formed. Such a complex may be free or immobilized (either covalently or noncovalently) on a support material. The ability to bind may generally be evaluated by determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind" in the context of the present invention when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known to those of ordinary skill in the art.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome with or without a peptide component, an RNA molecule or a peptide. In a preferred embodiment, the binding partner is an antibody, or a fragment thereof. Such antibodies may be polyclonal, or monoclonal. In addition, the antibodies may be single chain, chimeric, CDR-grafted or humanized. Antibodies may be prepared by the methods described herein and by other methods well known to those of skill in the art.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding partner to detect polypeptide markers in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In a preferred embodiment, the assay involves the use of binding partner immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a second binding partner that contains a reporter group. Suitable second binding partners include antibodies that bind to the binding partner/polypeptide complex. Alternatively, a competitive assay may be utilized, in which a

polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding partner after incubation of the binding partner with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding partner is indicative of the reactivity of the sample with the immobilized binding partner.

The solid support may be any material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 μ g, and preferably about 100 ng to about 1 μ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without prostate cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for prostate cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for prostate cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of prostate cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the antigens or antibodies of the present invention. The above descriptions are intended to be exemplary only.

In another embodiment, the above polypeptides may be used as markers for the progression of prostate cancer. In this embodiment, assays as described above for the diagnosis of prostate cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, prostate cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, prostate cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

Antibodies for use in the above methods may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g., Harlow and Lane, Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the antigenic polypeptide is initially injected into any of a wide variety of mammals (*e.g., mice, rats, rabbits, sheep and goats*). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e., reactivity with the polypeptide of interest*). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield,

such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Monoclonal antibodies of the present invention may also be used as therapeutic reagents, to diminish or eliminate prostate tumors. The antibodies may be used on their own (for instance, to inhibit metastases) or coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the

catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing

nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify prostate tumor-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a prostate tumor protein of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a prostate tumor protein of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule having a sequence provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis *et al. Ibid*; Ehrlich, *Ibid*). Primers or probes may

thus be used to detect prostate tumor-specific sequences in biological samples, including blood, semen, prostate tissue and/or prostate tumor tissue.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

Example 1

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A⁺ RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A⁺ RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA 94303), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor

library contained 1.64×10^7 independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained 3.3×10^6 independent colonies, with 69% of clones having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 μ g) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 μ l of H₂O, heat-denatured and mixed with 100 μ l (100 μ g) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 μ l) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 μ l H₂O to form the driver DNA.

To form the tracer DNA, 10 μ g prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 μ l H₂O. Tracer DNA was mixed with 15 μ l driver DNA and 20 μ l of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 μ l H₂O, mixed with 8 μ l driver DNA and 20 μ l of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into

BamHI/XhoI site of chloramphenicol resistant pBCSK⁺ (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (prostate subtraction 1).

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was

performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (prostate subtraction 2). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are

provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (prostate subtraction spike 2) was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (prostate subtraction 3). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS:

93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively. cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two novel clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

Example 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR
POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17, L1-12, F1-12 and N1-1862 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 μ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β -actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β -actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β -actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β -actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 and L1-12 appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in

prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17, N1-1862 and L1-12 are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 was detected in two prostate tumors and not in the other tissues tested. N1-1862 was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The micro-array technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal

colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Example 3

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO:41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO:46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no

significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. An additional clone, referred to as P703, was found to have five splice variants. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCT as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20 was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5

of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies using the above methodology resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, g-f12 and g-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, g-f12 and g-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequences of 7-g6 and g-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and g-f12 were found to show some homology to previously identified genes.

Example 4

SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Xu, Jiangchun
Dillin, Davin C.
- (ii) TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER
AND METHODS FOR THEIR USE
- (iii) NUMBER OF SEQUENCES: 224
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SEED and BERRY LLP
 - (B) STREET: 6300 Columbia Center, 701 Fifth Avenue
 - (C) CITY: Seattle
 - (D) STATE: WA
 - (E) COUNTRY: USA
 - (F) ZIP: 98104
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 23-FEB-1998
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Maki, David J.
 - (B) REGISTRATION NUMBER: 31,392
 - (C) REFERENCE/DOCKET NUMBER: 210121.427C3
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 622-4900
 - (B) TELEFAX: (206) 682-6031

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 814 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT	TTTTTCACAG	TATAACAGCT	CTTTATTTCT	GTGAGTTCTA	CTAGGAAATC	60
ATCAAATCTG	AGGGTTGTCT	GGAGGACTTC	AATACACCTC	CCCCCATAGT	GAATCAGCTT	120
CCAGGGGGTC	CAGTCCCTCT	CCTTACTTCA	TCCCCATCCC	ATGCCAAAGG	AAGACCCTCC	180
CTCCTTGGCT	CACAGCCTTC	TCTAGGCTTC	CCAGTGCCTC	CAGGACAGAG	TGGGTTATGT	240
TTTCAGCTCC	ATCCTTGCTG	TGAGTGTCTG	GTGCGTTGTG	CCTCCAGCTT	CTGCTCAGTG	300
CTTCATGGAC	AGTGTCCAGC	ACATGTCACT	CTCCACTCTC	TCAGTGTGGA	TCCACTAGTT	360
CTAGAGCGGC	CGCCACCGCG	GTGGAGCTCC	AGCTTTTGTG	CCCTTTAGTG	AGGGTTAATT	420

GCGCGCTTGG	CGTAATCATG	GTCATAACTG	TTTCCTGTGT	GAAATTGTTA	TCCGCTCACA	480
ATTCCACACA	ACATACGAGC	CGGAAGCATA	AAGTGTAAG	CCTGGGGTGC	CTAATGAGTG	540
ANCTAACTCA	CATTAATTGC	GTTCGCTCA	CTGNCCGCTT	TCCAGTCNGG	AAAACTGTCTG	600
TGCCAGCTGC	ATTAATGAAT	CGGCCAACGC	NCGGGGAAAA	GCGGTTTGCG	TTTGGGGGC	660
TCTTCCGCTT	CTCGCTCACT	NANTCCTGCG	CTCGGTCNTT	CGGCTGCGGG	GAACGGTATC	720
ACTCCTCAAA	GGNGGTATTA	CGGTTATCCN	NAAATCNGGG	GATACCCNGG	AAAAAANTTT	780
AACAAAAGGG	CANCAAAGGG	CNGAAACGTA	AAAA			814

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACAGAAATGT	TGGATGGTGG	AGCACCTTTC	TATACGACTT	ACAGGACAGC	AGATGGGGAA	60
TTTCATGGCTG	TTGGAGCAAT	AGAACCCAG	TTCTACGAGC	TGCTGATCAA	AGGACTTGGA	120
CTAAAGTCTG	ATGAACCTTC	CAATCAGATG	AGCATGGATG	ATTGGCCAGA	AATGAAGAAG	180
AAGTTTGCG	ATGTATTTGC	AAAGAAGACG	AAGGCAGAGT	GGTGTCAAAT	CTTTGACGGC	240
ACAGATGCCT	GTGTGACTCC	GGTTCTGACT	TTTGAGGAGG	TTGTTTCATCA	TGATCACAAC	300
AAGGAACGGG	GCTCGTTTAT	CACCACTGAG	GAGCAGGACG	TGAGCCCCCG	CCCTGCACCT	360
CTGCTGTTAA	ACACCCACAGC	CATCCCTTCT	TTCAAAGGG	ATCCACTAGT	TCTAGAAGCG	420
GCCGCCACCG	CGGTGGAGCT	CCAGCTTTTG	TTCCCTTTAG	TGAGGGTTAA	TTGCGCGCTT	480
GGCGTAATCA	TGGTCATAGC	TGTTTCCTGT	GTGAAATTGT	TATCCGCTCA	CAATTCCCCC	540
AACATACGAG	CCGGAACATA	AAGTGTTAAG	CCTGGGGTGC	CTAATGANTG	AGCTAACTCN	600
CATTAATTGC	GTTCGCTCA	CTGCCGCTT	TCCAGTCGGG	AAAACTGTCG	TGCCACTGCN	660
TTANTGAATC	NGCCACCCCC	CGGAAAAGG	CGGTTGCTNTT	TTGGGCCTCT	TCCGCTTTCC	720
TCGCTCATTG	ATCCTNGCNC	CCGGTCTTCG	GCTGCGNGA	ACGGTTCACT	CCTCAAAGGC	780
GGTNTNCCGG	TTATCCCCAA	ACNGGGGATA	CCNGA			816

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTTTGAAAG	AAGGGATGGC	TGGGGTGTTT	AACAGCAGAG	GTGCAGGGCG	GGGGCTCACG	60
TCCTGCTCCT	CACTGGTGAT	AAACGAGCCC	CGTTCCTTGT	TGTGATCATG	ATGAACAACC	120
TCCTCAAAAG	TCAGAACCGG	AGTCACACAG	GCATCTGTGC	CGTCAAAGAT	TTGACACCAC	180
TCTGCCTTCG	TCTTCTTTGC	AAATACATCT	GCAAACTTCT	TCTTCATTTC	TGGCCAATCA	240
TCCATGCTCA	TCTGATTGGG	AAGTTCATCA	GACTTTAGTC	CANNTCCTTT	GATCAGCAGC	300
TCGTAGAACT	GGGGTTCTAT	TGCTCCAACA	GCCATGAATT	CCCCATCTGC	TGTCCTGTAA	360
GTCGTATAGA	AAGGTGCTCC	ACCATCCAAC	ATGTTCTGTC	CTCGAGGGGG	GGCCCGGTAC	420
CCAATTTCGCC	CTATANTGAG	TCGTATTACG	CGCGCTCACT	GGCCGTCGTT	TTACAACGTC	480
GTGACTGGGA	AAACCCTGGG	CGTTACCAAC	TTAATCGCCT	TGCAGCACAT	CCCCCTTTCG	540
CCAGCTGGGC	GTAATANCGA	AAAGGCCCGC	ACCGATCGCC	CTTCCAACAG	TTGCGCACCT	600
GAATGGGNAA	ATGGGACCCC	CCTGTTACCG	CGCATTNAAAC	CCCCGCNNGG	TTTNGTTGTT	660
ACCCCCACNT	NNACCGCTTA	CACTTTGCCA	GCGCCTTANC	GCCCGCTCCC	TTTCNCCTTT	720
CTTCCCTTCC	TTTCNCNCCN	CTTTCCCCCG	GGGTTTCCCC	CNTCAAACCC	CNA	773

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 828 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTCCTGAGT	CCTACTGACC	TGTGCTTTCT	GGTGTGGAGT	CCAGGGCTGC	TAGGAAAAGG	60
AATGGGCAGA	CACAGGTGTA	TGCCAATGTT	TCTGAAATGG	GTATAATTTC	GTCTCTCCT	120
TCGGAACACT	GGCTGTCTCT	GAAGACTTCT	CGCTCAGTTT	CAGTGAGGAC	ACACACAAAG	180
ACGTGGGTGA	CCATGTTGTT	TGTGGGGTGC	AGAGATGGGA	GGGTGGGGC	CCACCCTGGA	240
AGAGTGGACA	GTGACACAAG	GTGGACACTC	TCTACAGATC	ACTGAGGATA	AGCTGGAGCC	300
ACAATGCATG	AGGCACACAC	ACAGCAAGGA	TGACNCTGTA	AACATAGCCC	ACGCTGTCCT	360
GNGGGCACTG	GGAAGCCTAN	ATNAGGCCGT	GAGCANAAAG	AAGGGGAGGA	TCCACTAGTT	420
CTANAGCGGC	CGCCACCGCG	GTGGANCTCC	ANCTTTTGTT	CCCTTAGTG	AGGGTTAATT	480
GCGCGCTTGG	CNTAATCATG	GTCATANCTN	TTTCCTGTGT	GAAATGTGTA	TCCGCTCACA	540
ATTCCACACA	ACATACGANC	CGGAAACATA	AANTGTAAAC	CTGGGGTGCC	TAATGANTGA	600
CTAACTCACA	TTAATTGCGT	TGCGCTCACT	GCCCGCTTTC	CAATCNGGAA	ACCTGTCTTG	660
CCNCTTGCA	TNATGAATCN	GCCAACCCCC	GGGAAAAGC	GTTTGCGTTT	TGGGCGCTCT	720
TCCGCTTCCT	CNCTCANTTA	NTCCCTNCNC	TCGGTCATTC	CGGCTGCNGC	AAACCGGTTC	780
ACCNCCTCCA	AAGGGGTAT	TCCGGTTTCC	CCNAATCCGG	GGANANCC		828

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 834 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTTTTTTTT	TTTTTACTGA	TAGATGGAAT	TTATTAAGCT	TTTCACATGT	GATAGCACAT	60
AGTTTTTAAT	GCATCCAAAG	TACTAACAAA	AACTCTAGCA	ATCAAGAATG	GCAGCATGTT	120
ATTTTATAAC	AATCAACACC	TGTGGCTTTT	AAAATTTGGT	TTTCATAAGA	TAATTTATAC	180
TGAAGTAAAT	CTAGCCATGC	TTTTAAAAAA	TGCTTTAGGT	CACTCCAAGC	TTGGCAGTTA	240
ACATTTGGCA	TAAACAATAA	TAAAACAATC	ACAATTTAAT	AAATAACAAA	TACAACATTG	300
TAGGCCATAA	TCATATACAG	TATAAGGAAA	AGGTGGTAGT	GTTGAGTAAG	CAGTTATTAG	360
AATAGAATAC	CTTGGCCTCT	ATGCAAATAT	GTCTAGACAC	TTTGATTAC	TCAGCCCTGA	420
CATTCAGTTT	TCAAAGTAGG	AGACAGGTTC	TACAGTATCA	TTTTACAGTT	TCCAACACAT	480
TGAAAACAAG	TAGAAAATGA	TGAGTTGATT	TTTATTAATG	CATTACATCC	TCAAGAGTTA	540
TCACCAACCC	CTCAGTTATA	AAAAATTTTC	AAGTTATATT	AGTCATATAA	CTTGGTGTGC	600
TTATTTTAAA	TTAGTGCTAA	ATGGATTAA	TGAAGACAAC	AATGGTCCCC	TAATGTGATT	660
GATATTGGTC	ATTTTACCA	GCTTCTAAAT	CTNAACTTTC	AGGCTTTTGA	ACTGGAACAT	720
TGNATNACAG	TGTTCCANAG	TTNCAACCTA	CTGGAACATT	ACAGTGTGCT	TGATTCAAAA	780
TGTTATTTTG	TTAAAAATTA	AATTTTAACC	TGGTGGAAAA	ATAATTTGAA	ATNA	834

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 818 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTTTTTTTT	TTTTTTTTTT	AAGACCCCTCA	TCAATAGATG	GAGACATACA	GAAATAGTCA	60
AACCACATCT	ACAAAATGCC	AGTATCAGGC	GGCGGCTTCG	AAGCCAAAGT	GATGTTTGGA	120
TGTAAAGTGA	AATATTAGTT	GGCGGATGAA	GCAGATAGTG	AGGAAAAGTTG	AGCCAATAAT	180
GACGTGAAGT	CCGTGGAAGC	CTGTGGCTAC	AAAAAATGTT	GAGCCGTAGA	TGCCGTCGGA	240
AATGGTGAAG	GGAGACTCGA	AGTACTCTGA	GGCTTGTAGG	AGGGTAAAT	AGAGACCCAG	300
TAAAATTGTA	ATAAGCAGTG	CTTGAATTAT	TTGGTTTCGG	TTGTTTTCTA	TTAGACTATG	360
GTGAGCTCAG	GTGATTGATA	CTCCTGATGC	GAGTAATACG	GATGTGTTTA	GGAGTGGGAC	420
TTCTAGGGGA	TTTAGCGGGG	TGATGCCTGT	TGGGGGCCAG	TGCCCTCCTA	GTTGGGGGGT	480
AGGGGCTAGG	CTGGAGTGGT	AAAAGGCTCA	GAAAAATCCT	GCGAAGAAAA	AAACTTCTGA	540
GGTAATAAAT	AGGATTATCC	CGTATCGAAG	GCCTTTTGG	ACAGGTGGTG	TGTGGTGGCC	600
TTGGTATGTG	CTTTCTCGTG	TTACATCGCG	CCATCATTGG	TATATGGTTA	GTGTGTTGGG	660
TTANTANGGC	CTANTATGAA	GAACCTTTTG	ANTGGAATTA	AATCAATNGC	TTGGCCGGAA	720
GTCATTANGA	NGGCTNAAAA	GGCCCTGTTA	NGGGTCTGGG	CTNGGTTTAA	CCCNACCCAT	780
GGAATNCNCC	CCCCGGACNA	NTGNATCCCT	ATTCTTAA			818

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTTTTTTTT	TTTTTTTTTT	TGGCTCTAGA	GGGGGTAGAG	GGGGTGCTAT	AGGGTAAATA	60
CGGGCCCTAT	TTCAAAGATT	TTTAGGGGAA	TTAATTCTAG	GACGATGGGT	ATGAAACTGT	120
GGTTTGCTCC	ACAGATTTCA	GAGCATTGAC	CGTAGTATAC	CCCCGGTCGT	GTAGCGGTGA	180
AAGTGGTTTG	GTTTAGACGT	CCGGGAATTG	CATCTGTTT	TAAGCCTAAT	GTGGGGACAG	240
CTCATGAGTG	CAAGACGTCT	TGTGATGTAA	TTATTATACN	AATGGGGGCT	TCAATCGGGA	300
GTACTACTCG	ATTGTCAACG	TCAAGGAGTC	GCAGGTCGCC	TGGTTCTAGG	AATAATGGGG	360
GAAGTATGTA	GGAATTGAAG	ATTAATCCGC	CGTAGTCGGT	GTTCTCCTAG	GTTCAATACC	420
ATTGGTGGCC	AATTGATTTG	ATGGTAAGGG	GAGGGATCGT	TGAACTCGTC	TGTTATGTAA	480
AGGATNCCTT	NGGGATGGGA	AGGCNATNAA	GGACTANGGA	TNAATGGCGG	GCANGATATT	540
TCAAACNGTC	TCTANTTCCT	GAAACGTCTG	AAATGTTAAT	AANAATTAA	TTTNGTTATT	600
GAATNTTNG	GAAAAGGGCT	TACAGGACTA	GAAACCAAAT	ANGAAAANTA	ATNNTAANGG	660
CNTTATCNTN	AAAGGTNATA	ACCNCTCCTA	TNATCCCACC	CAATNGNATT	CCCCACNCNN	720
ACNATTGGAT	NCCCCANTTC	CANAAANGGC	CNCCCCCGG	TGNANNCCNC	CTTTTGTTCC	780
CTTNANTGAN	GGTTATTNC	CCCTNGCNTT	ATCANCC			817

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATTTCCGGG	TTTACTTTCT	AAGGAAAGCC	GAGCGGAAGC	TGCTAACGTG	GGAATCGGTG	60
CATAAGGAGA	ACTTTCTGCT	GGCACGCGCT	AGGGACAAGC	GGGAGAGCGA	CTCCGAGCGT	120

CTGAAGCGCA	CGTCCCAGAA	GGTGGACTTG	GCACTGAAAC	AGCTGGGACA	CATCCGCGAG	180
TACGAACAGC	GCCTGAAAGT	GCTGGAGCGG	GAGGTCCAGC	AGTGTAGCCG	CGTCCTGGGG	240
TGGGTGGCCG	ANGCCTGANC	CGCTCTGCCT	TGCTGCCCCC	ANGTGGGCCG	CCACCCCTG	300
ACCTGCCTGG	GTCCAAACAC	TGAGCCCTGC	TGGCGGACTT	CAAGGANAAC	CCCCACANGG	360
GGATTTTGCT	CCTANANTAA	GGCTCATCTG	GGCCTCGGCC	CCCCCACCTG	GTTGGCCTTG	420
TCTTTGANGT	GAGCCCCATG	TCCATCTGGG	CCACTGTCNG	GACCACCTTT	NGGGAGTGTT	480
CTCCTTACAA	CCACANNATG	CCCGGCTCCT	CCCGGAAACC	ANTCCCANCC	TGNGAAGGAT	540
CAAGNCCTGN	ATCCACTNNT	NCTANAACCG	GCCNCCNCCG	CNGTGGAAACC	CNCCTTNTGT	600
TCCTTTTCNT	TNAGGGTTAA	TNNCGCCTTG	GCCTTNCCAN	NGTCCTNCNC	NTTTTCCNNT	660
GTTNAAATTG	TTANGCNCCC	NCCNNTCCCN	CNNCNCNAN	CCCGACCCNN	ANNTTNNANN	720
NCCTGGGGGT	NCCNNCNGAT	TGACCCNNCC	NCCCTNTANT	TGCNTTNGGG	NNCNNTGCC	780
CTTTCCCTCT	NGGGANNCG					799

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGCCTTGAT	CCTCCCAGGC	TGGGACTGGT	TCTGGGAGGA	GCCGGGCATG	CTGTGGTTTG	60
TAANGATGAC	ACTCCCAAAG	GTGGTCCTGA	CAGTGGCCCA	GATGGACATG	GGGCTCACCT	120
CAAGGACAAG	GCCACCAGGT	GCGGGGGCCG	AAGCCCACAT	GATCCTTACT	CTATGAGCAA	180
AATCCCCTGT	GGGGGCTTCT	CCTTGAAGTC	CGCCANCAGG	GCTCAGTCTT	TGGACCCANG	240
CAGGTCATGG	GGTTGTNGNC	CAACTGGGGG	CCNCAACGCA	AAANGGCNCA	GGGCCTCNGN	300
CACCCATCCC	ANGACGCGGC	TACACTNCTG	GACCTCCCNC	TCCACCACTT	TCATGCGCTG	360
TTCNTACCCG	CGNATNTGTC	CCANCTGTTT	CNGTGCCNAC	TCCANCTTCT	NGGACGTGCG	420
CTACATACGC	CCGGANTCNC	NCTCCCGCTT	TGTCCTTATC	CACGTNCCAN	CAACAAATTT	480
CNCCNTANTG	CACCNATTCC	CACNTTTNNC	AGNTTTCNC	NNCGNGCTTC	CTTNTAAAAG	540
GGTTGANCCC	CGGAAAATNC	CCCAAAGGGG	GGGGGCCNGG	TACCCAACTN	CCCCCTNATA	600
GCTGAANTCC	CCATNACCNN	GNCTCNATGG	ANCCNTCCNT	TTTAANNACN	TTCTNAACTT	660
GGGAANANCC	CTCGNCCNTN	CCCCNTTAA	TCCCNCCCTG	CNANGNNCNT	CCCCCNNTCC	720
NCCCNNTTNG	GCNTNTNANN	CNAAAAGGC	CCNNNANCAA	TCTCCTNNCN	CCTCANTTCG	780
CCANCCCTCG	AAATCGGCCN	C				801

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGTCTATNT	GGCCAGTGTG	GCAGCTTTCC	CTGTGGCTGC	CGGTGCCACA	TGCCTGTCCC	60
ACAGTGTGGC	CGTGGTGACA	GCTTCAGCCG	CCCTCACC GG	GTTACCTTC	TCAGCCCTGC	120
AGATCCTGCC	CTACACACTG	GCCTCCCTCT	ACCACCGGGA	GAAGCAGGTG	TTCTGCCCCA	180
AATACCGAGG	GGACACTGGA	GGTGCTAGCA	GTGAGGACAG	CCTGATGACC	AGCTTCCTGC	240
CAGGCCCTAA	GCCTGGAGCT	CCCTTCCCTA	ATGGACACGT	GGGTGCTGGA	GGCAGTGCC	300
TGCTCCCACC	TCCACCCGCG	CTCTGCGGGG	CCTCTGCCTG	TGATGTCTCC	GTACGTGTGG	360
TGGTGGGTGA	GCCCACCGAN	GCCAGGGTGG	TTCCGGGCGG	GGGCATCTGC	CTGGACCTCG	420
CCATCCTGGA	TAGTGCTTCC	TGCTGTCCCA	NGTGGCCCCA	TCCCTGTTTA	TGGGCTCCAT	480
TGTCCAGCTC	AGCCAGTCTG	TCACTGCCTA	TATGGTGTCT	GCCGCAGGCC	TGGGTCTGGT	540

CCCATTACT	TTGCTACACA	GGTANTATTT	GACAAGAACG	ANTTGGCCAA	ATACTCAGCG	600
TTAAAAAATT	CCAGCAACAT	TGGGGGTGGA	AGGCCTGCCT	CACTGGGTCC	AACTCCCCGC	660
TCCTGTTAAC	CCCATGGGGC	TGCCGGCTTG	GCCGCCAATT	TCTGTTGCTG	CCAAANTNAT	720
GTGGCTCTCT	GCTGCCACCT	GTGCTGGCT	GAAGTGCNTA	CNGCNCANCT	NGGGGGGTNG	780
GGNGTTCCC						789

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCCACCCTAC	CCAAATATTA	GACACCAACA	CAGAAAAGCT	AGCAATGGAT	TCCCTTCTAC	60
TTTGTTAAAT	AAATAAGTTA	AATATTTAAA	TGCCTGTGTC	TCTGTGATGG	CAACAGAAGG	120
ACCAACAGGC	CACATCCTGA	TAAAAGGTAA	GAGGGGGGTG	GATCAGCAAA	AAGACAGTGC	180
TGTGGGCTGA	GGGGACCTGG	TTCTTGTGTG	TTGCCCTCA	GGACTCTTCC	CCTACAAATA	240
ACTTTCATAT	GTTCAAATCC	CATGGAGGAG	TGTTTCATCC	TAGAAACTCC	CATGCAAGAG	300
CTACATTAAA	CGAAGCTGCA	GGTTAAGGGG	CTTANAGATG	GGAAACCAGG	TGACTGAGTT	360
TATTCAGCTC	CCAAAAACCC	TTCTCTAGGT	GTGTCTCAAC	TAGGAGGCTA	GCTGTTAACC	420
CTGAGCCTGG	GTAATCCACC	TGCAGAGTCC	CCGCATCCA	GTGCATGGAA	CCCTTCTGGC	480
CTCCCTGTAT	AAGTCCAGAC	TGAAACCCCC	TTGGAAGGNC	TCCAGTCAGG	CAGCCCTANA	540
AACTGGGGAA	AAAAGAAAAG	GACGCCCCAN	CCCCAGCTG	TGCANCTACG	CACCTCAACA	600
GCACAGGGTG	GCAGCAAAAA	AACCACTTTA	CTTTGGCACA	AACAAAAACT	NGGGGGGGCA	660
ACCCCGGCAC	CCCNANGGGG	GTTAACAGGA	ANCNGGGNAA	CNTGGAACCC	AATTNAGGCA	720
GGCCCNCCAC	CCCNAAATNTT	GCTGGGAAAT	TTTTCTCTCC	CTAAATTNTT	TC	772

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCCCCAATTC	CAGCTGCCAC	ACCACCCACG	GTGACTGCAT	TAGTTCGGAT	GTCATACAAA	60
AGCTGATTGA	AGCAACCCTC	TACTTTTTTG	TCGTGAGCCT	TTTGCTTGGT	GCAGGTTTCA	120
TGGCTGTGT	TGGTGACGTT	GTCAATTGCAA	CAGAATGGGG	GAAAGGCAC	GTTCTCTTTG	180
AAGTANGGTG	AGTCCCTCAA	ATCCGTATAG	TTGGTGAAGC	CACAGCACTT	GAGCCCTTTC	240
ATGGTGGTGT	TCCCACTTGT	AGTGAAGTCT	TCCTGGGAAC	CATAATCTTT	CTTGATGGCA	300
GGCACTACCA	GCAACGTCAG	GGAAGTGCTC	AGCCATTGTG	GTGTACACCA	AGGCGACCAC	360
AGCAGCTGCN	ACCTCAGCAA	TGAAGATGAN	GAGGANGATG	AAGAAGAACG	TCNCGAGGGC	420
ACACTTGCTC	TCAGTCTTAN	CACCATANCA	GCCCNTGAAA	ACCAANANCA	AAGACCACNA	480
CNCCGGCTGC	GATGAAGAAA	TNACCCNCG	TTGACAAACT	TGCATGGCAC	TGGGANCCAC	540
AGTGGCCCN	AAAATCTTCA	AAAAGGATGC	CCCATCNATT	GACCCCCCAA	ATGCCCACTG	600
CCAACAGGGG	CTGCCCCACN	CNCNNAACGA	TGANCCNATT	GNACAAGATC	TNCNTGGTCT	660
TNATNAACNT	GAACCCTGCN	TNGTGGCTCC	TGTTTCAGGNC	CNNGGCCTGA	CTTCTNAANN	720
AANGAACTCN	GAAGNCCCCA	CNGGANANNC	G			751

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCCAGGCG	TCCCTCTGCC	TGCCCCACTCA	GTGGCAACAC	CCGGGAGCTG	TTTTGTCCTT	60
TGTGGANCC	CAGCAGTNC	CTCTTTTCA	ACTCANTGCC	AAGANCCCTG	AACAGGAGCC	120
ACCATGCAGT	GCTTCAGCTT	CATTAAAGAC	ATGATGATCC	TCTTCAATTT	GCTCATCTTT	180
CTGTGTGGTG	CAGCCCTGTT	GGCAGTGGGC	ATCTGGGTGT	CAATCGATGG	GGCATCCTTT	240
CTGAAGATCT	TCGGGCCACT	GTCGTCCAGT	GCCATGCAGT	TTGTCAACGT	GGGCTACTTC	300
CTCATCGCAG	CCGGCGTTGT	GGTCTTAGCT	CTAGGTTTCC	TGGGCTGCTA	TGGTGCTAAG	360
ACTGAGAGCA	AGTGTGCCCT	CGTGACGTT	TTCTTCATCC	TCCTCCTCAT	CTTCATTGCT	420
GAGGTTGCAA	TGCTGTGGTC	GCCTTGGTGT	ACACCACAAT	GGCTGAGCAC	TTCCTGACGT	480
TGCTGGTAAT	GCCTGCCATC	AANAAAAGAT	TATGGGTTCC	CAGGAANACT	TCACTCAAGT	540
GTTGGAAACAC	CACCATGAAA	GGGCTCAAGT	GCTGTGGCTT	CNNCCAATA	TACGGATTTT	600
GAAGANTCAC	CTACTTCAAA	GAAAANAGTG	CCTTTCCCCC	ATTTCTGTTG	CAATTGACAA	660
ACGTCCCCAA	CACAGCCAAT	TGAAAACCTG	CACCCAACCC	AAANGGGTCC	CCAACCANAA	720
ATTNAAGGG						729

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTCTTCCT	CAAAGTTGTT	CTTGTTGCCA	TAACAACCAC	CATAGGTAAA	GCGGGCGCAG	60
TGTTGCTGA	AGGGGTTGTA	GTACCAGCGC	GGGATGCTCT	CCTTGCAGAG	TCCTGTGTCT	120
GGCAGGTCCA	CGCAGTGCCC	TTTGTCAC	TGGGAAATGGA	TGCGCTGGAG	CTCGTCAAAG	180
CCACTCGTGT	ATTTTTCACA	GGCAGCCTCG	TCCGACGCGT	CGGGGCAGTT	GGGGGTGTCT	240
TCACACTCCA	GGAAACTGTC	NATGCAGCAG	CCATTGCTGC	AGCGGAACTG	GGTGGGCTGA	300
CANGTGCCAG	AGCACACTGG	ATGGCGCCTT	TCCATGNNAN	GGGCCCTGNG	GGAAAGTCCC	360
TGANCCCCAN	ANCTGCCTCT	CAAANGCCCC	ACCTTGACAC	CCCCGACAGG	CTAGAATGGA	420
ATCTTCTTCC	CGAAAGGTAG	TTNTTCTTGT	TGCCCAANCC	ANCCCCNTAA	ACAAACTCTT	480
GCANATCTGC	TCCGNGGGGG	TCNTANTACC	ANCGTGGGAA	AAGAACCCCA	GGCNGCGAAC	540
CAANCTTGTT	TGGATNCGAA	GCNATAATCT	NCTNTTCTGC	TTGGTGGACA	GCACCANTNA	600
CTGTNNANCT	TTAGNCCNTG	GTCCTCNTGG	GTTGNNTCTG	AACCTAATCN	CCNNTCAACT	660
GGGACAAGGT	AANTNGCCNT	CCTTTNAATT	CCCNANCNTN	CCCCCTGGTT	TGGGGTTTTN	720
CNCNCTCCTA	CCCCAGAAAN	NCCGTGTTCC	CCCCCAACTA	GGGGCCNAAA	CCNNTTNTTC	780
CACAACCTN	CCCCACCCAC	GGGTTGNGNT	GGTGTTG			816

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCAAGGCCTG	GGCAGGCATA	NACCTGAAGG	TACAACCCCA	GGAACCCCTG	GTGCTGAAGG	60
ATGTGGAAAA	CACAGATTGG	CGCCTACTGC	GGGGTGACAC	GGATGTCAGG	GTAGAGAGGA	120
AAGACCCAAA	CCAGGTGGAA	CTGTGGGGAC	TCAAGGAANG	CACCTACCTG	TCCAGCTGA	180
CAGTGACTAG	CTCAGACCAC	CCAGAGGACA	CGGCCAACGT	CACAGTCACT	GTGCTGTCCA	240
CCAAGCAGAC	AGAAGACTAC	TGCCTCGCAT	CCAACAANGT	GGGTCGCTGC	CGGGGCTCTT	300
TCCACGCTG	GTACTATGAC	CCCACGGAGC	AGATCTGCAA	GAGTTTCGTT	TATGGAGGCT	360
GCTTGGGCAA	CAAGAACAAC	TACCTTCGGG	AAGAAGAGTG	CATTCTANCC	TGTCNNGGTG	420
TGCAAGGTGG	GCCTTTGANA	NGCANCTCTG	GGGCTCANGC	GACTTTCCCC	CAGGGCCCCCT	480
CCATGGAAAG	GCGCCATCCA	NTGTTCTCTG	GCACCTGTCA	GCCCACCCAG	TTCCGCTGCA	540
NCAATGGCTG	CTGCATCNAC	ANTTTCCTNG	AATTGTGACA	ACACCCCCCA	NTGCCCCCAA	600
CCCTCCCAAC	AAAGCTTCCC	TGTTNAAAAA	TACNCCANTT	GGCTTTTNAC	AAACNCCCGG	660
CNCCTCCNTT	TTCCCCNNTN	AACAAAGGGC	NCTNGCNTTT	GAAGTCCCN	AACCCNGGAA	720
TCTNCCNNGG	AAAAANTNCC	CCCCCTGGTT	CCTNNAANCC	CCTCCNCNAA	ANCTNCCCCC	780
CCC						783

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCCCCAATTC	CAGCTGCCAC	ACCACCCACG	GTGACTGCAT	TAGTTCGGAT	GTCATACAAA	60
AGCTGATTGA	AGCAACCCCTC	TACTTTTGG	TCGTGAGCCT	TTTGCTTGGT	GCAGGTTTCA	120
TGGCTGTGT	TGGTGACGTT	GTCAATGCAA	CAGAATGGGG	GAAAGGCACT	GTTCTCTTTG	180
AAGTAGGGTG	AGTCCTCAAA	ATCCGTATAG	TTGGTGAAGC	CACAGCACTT	GAGCCCTTTC	240
ATGGTGGTGT	TCCACACTTG	AGTGAAGTCT	TCCTGGGAAC	CATAATCTTT	CTTGATGGCA	300
GGCACTACCA	GCAACGTCAG	GAAGTGCTCA	GCCATTGTGG	TGTACACCAA	GGCGACCACA	360
GCAGCTGCAA	CCTCAGCAAT	GAAGATGAGG	AGGAGGATGA	AGAAGAACGT	CNCGAGGGCA	420
CACTTGCTCT	CCGTCTTAGC	ACCATAGCAG	CCCANGAAAC	CAAGAGCAAA	GACCACAACG	480
CCNGCTGCGA	ATGAAAGAAA	NTACCCACGT	TGACAACTG	CATGGCCACT	GGACGACAGT	540
TGGCCCGAAN	ATCTTCAGAA	AAGGGATGCC	CCATCGATTG	AACACCCANA	TGCCCCACTGC	600
CNACAGGGCT	GCNCCNCNCN	GAAAGAATGA	GCCATTGAAG	AAGGATCNTC	NTGGTCTTAA	660
TGAAGTGAAG	CCNTGCATGG	TGGCCCCCTGT	TCAGGGCTCT	TGGCAGTGAA	TTCTGANAAA	720
AAGGAACNGC	NTNAGCCCCC	CCAAANGANA	AAACACCCCC	GGGTGTTGCC	CTGAATTGGC	780
GGCCAAGGAN	CCCTGCCCCN	G				801

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTGAGAGCCA	GGCGTCCCTC	TGCCTGCCCA	CTCAGTGGCA	ACACCCGGGA	GCTGTTTTGT	60
CCTTTGTGGA	GCCTCAGCAG	TTCCCTCTTT	CAGAATCAC	TGCCAAGAGC	CCTGAACAGG	120
AGCCACCATG	CAGTGCTTCA	GCTTCATTAA	GACCATGATG	ATCCTCTTCA	ATTTGCTCAT	180
CTTTCTGTGT	GGTGCAGCCC	TGTTGGCAGT	GGGCATCTGG	GTGTCAATCG	ATGGGGCATC	240
CTTTCTGAAG	ATCTTCGGGC	CACTGTCTGC	CAGTGCCATG	CAGTTTGTCA	ACGTGGGCTA	300
CTTCTCATC	GCAGCCGGCG	TTGTGGTCTT	TGCTCTTGGT	TTCCTGGGCT	GCTATGGTGC	360

TAAGACGGAG	AGCAAGTGTG	CCCTCGTGAC	GTTCTTCTTC	ATCCTCCTCC	TCATCTTCAT	420
TGCTGAAGTT	GCAGCTGCTG	TGGTCGCCTT	GGTGACACC	ACAATGGCTG	AACCATTCTT	480
GACGTTGCTG	GTANTGCCTG	CCATCAANAA	AGATTATGGG	TTCCCAGGAA	AAATTCACTC	540
AANTNTGGAA	CACCNCCATG	AAAAGGGCTC	CAATTCTGN	TGGCTTCCCC	AACTATACCG	600
GAATTTTGAA	AGANTCNCCC	TACTTCCAAA	AAAAAANANT	TGCCTTNCC	CCCNTTCTGT	660
TGCAATGAAA	ACNTCCCAAN	ACNGCCAATN	AAAACCTGCC	CNNNCAAAAA	GGNTCNCAAA	720
CAAAAAAANT	NNAAGGGTTN					740

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCGCTGGTTG	CGCTGGTCCA	GNGNAGCCAC	GAAGCACGTC	AGCATACACA	GCCTCAATCA	60
CAAGGTCTTC	CAGCTGCCGC	ACATTACGCA	GGGCAAGAGC	CTCCAGCAAC	ACTGCATATG	120
GGATACACTT	TACTTTAGCA	GCCAGGGTGA	CAACTGAGAG	GTGTCGAAGC	TTATTCTTCT	180
GAGCCTCTGT	TAGTGGAGGA	AGATTCCGGG	CTTCAGCTAA	GTAGTCAGCG	TATGTCCCAT	240
AAGCAAACAC	TGTGAGCAGC	CGGAAGGTAG	AGGCAAAGTC	ACTCTCAGCC	AGCTCTCTAA	300
CATTGGGCAT	GTCCAGCAGT	TCTCCAAACA	CGTAGACACC	AGNGGCCTCC	AGCACCTGAT	360
GGATGAGTGT	GGCCAGCGCT	GCCCCCTTGG	CCGACTTGGC	TAGGAGCAGA	AATTGCTCCT	420
GGTTCTGCCC	TGTCACCTTC	ACTTCCGCAC	TCATCACTGC	ACTGAGTGTG	GGGGACTTGG	480
GCTCAGGATG	TCCAGAGACG	TGTTCCGCC	CCCTCNCTTA	ATGACACCGN	CCANNCAACC	540
GTCGGCTCCC	GCCGANTGNG	TTCGTCGTNC	CTGGGTCAGG	GTCTGCTGGC	CNCTACTTGC	600
AANCTTCGTC	NGGCCCCATG	AATTCACCNC	ACCGGAACTN	GTANGATCCA	CTNNTTCTAT	660
AACCGNCGC	CACCGCNNNT	GGAATCCAC	TCTTNTNCC	TTTACTTGAG	GGTTAAGGTC	720
ACCTTNNCG	TTACCTTGGT	CCAAACCNTN	CCNTGTGTG	ANATNGTNAA	TCNGGNCCNA	780
TNCCANCCNC	ATANGAAGCC	NG				802

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CNAAGCTTCC	AGGTNACGGG	CCGCNAANCC	TGACCCNAGG	TANCANAANG	CAGNCNGCGG	60
GAGCCCACCG	TCACGNGGNG	GNGTCTTTAT	NGGAGGGGGC	GGAGCCACAT	CNCTGGACNT	120
CNTGACCCCA	ACTCCCCNCC	NCNCANTGCA	GTGATGAGTG	CAGAAGTAA	GGTNACGTGG	180
CAGGAACCAA	GANCAANNC	TGCTCCNNTC	CAAGTCGGCN	NAGGGGGCGG	GGCTGGCCAC	240
GCNCATCCNT	CNAGTGCTGN	AAAGCCCCNN	CCTGTCTACT	TGTTTGGAGA	ACNGCNNNGA	300
CATGCCCAGN	GTTANATAAC	NGGCNGAGAG	TNANTTTGCC	TCTCCCTTCC	GGCTGCGCAN	360
CGNGTNTGCT	TAGNGGACAT	AACCTGACTA	CTTAAGTAA	CCCNNGAATC	TNCCNCCCCT	420
CCACTAAGCT	CAGAACAAAA	AACTTCGACA	CCACTCANTT	GTCACCTGNC	TGCTCAAGTA	480
AAGTGTAACC	CATNCCCAAT	GTNTGCTNGA	NGCTCTGNCC	TGCNTTANGT	TCGGTCCTGG	540
GAAGACCTAT	CAATTNAAGC	TATGTTTCTG	ACTGCCTCTT	GCTCCCTGNA	ACAANCNACC	600
CNNCNNTCCA	AGGGGGGGNC	GGCCCCCAAT	CCCCCAACC	NTNAATTNAN	TTTANCCCCN	660
CCCCNNGGCC	CGGCCTTTTA	CNANCNTCNN	NNACNGGGNA	AAACCNNNGC	TTTNCCTAAC	720
NNAATCCNCC	T					731

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTTTTTTTTT	TTTTTTTTTT	TAAAAACCCC	CTCCATTNAA	TGNAAACTTC	CGAAATTGTC	60
CAACCCCTC	NTCCAAATNN	CCNTTTCGG	GNGGGGGTTC	CAAACCCAAN	TTANNTTGG	120
ANNTTAAATT	AAATNTTNN	TGGNGGNNNA	ANCCNAATGT	NANGAAAGTT	NAACCCANTA	180
TNANCTTNA	TNCCTGAAA	CCNGTNGNTT	CCAAAAATNT	TTAACCCCTTA	ANTCCCTCCG	240
AAATNGTTNA	NGGAAAACCC	AAATTTCTCNT	AAGGTTGTTT	GAAGGNTNAA	TNAAAANCCC	300
NNCCAATTGT	TTTTNGCCAC	GCCTGAATTA	ATTGGNTTCC	GNTGTTTTCC	NTTAAAAANAA	360
GGNNANCCCC	GGTTANTNAA	TCCCCCCNNC	CCCAATTATA	CCGANTTTTT	TTNGAATTGG	420
GANCCCNCGG	GAATTAACGG	GGNNNNTCCC	TNTTGGGGGG	CNGGNNCCCC	CCCCNTCGGG	480
GGTTNGGGNC	AGGNCNNAAT	TGTTTAAAGG	TCCGAAAAAT	CCCTCCNAGA	AAAAAANCTC	540
CCAGGNTGAG	NNTNGGGTTT	NCCCCCCCCC	CANGCCCCCT	CTCGNANAGT	TGGGGTTTGG	600
GGGGCCTGGG	ATTTTNTTTC	CCCTNTTNCC	TCCCCCCCCC	CCNGGGANAG	AGGTTNGNGT	660
TTTGNTCNNC	GGCCCCNCCN	AAGANCTTTN	CCGANTTNAN	TTAAATCCNT	GCCTNGGCGA	720
AGTCNTTGN	AGGGNTAAAN	GGCCCCCTNN	CGGG			754

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 755 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATCANCCCAT	GACCCCNAA	C	NGGGACCC	NC	TCANCCGGNC	NNNCNACCNC	CGGCCNATCA	60
NNGTNAGNNC	ACTNCNNTN	N	NATCACNCCC	C	CNCCNACTAC	CCCCNCNANC	CNACGCNCTA	120
NNCANATNCC	ACTGANNGCG	C	CGANGTNGAN	N	AGAGAAANCT	NATACCANAG	NCACCANACN	180
CCAGCTGTCC	NANAANGCCT	N	NNNATACNGG	N	NNNATCCAAT	NTGNANCCTC	CNAAGTATTN	240
NNCNANANAT	GATTTTCCCTN	A	ANCCGATTAC	C	CCNTNCCCCC	TANCCCCCTCC	CCCCCAACNA	300
CGAAGGCNCT	GGNCCNAAGG	N	NGGCGNCNCC	C	CGCTAGNTC	CCCNNCAAGT	CNCNCNCCTA	360
AACTCANCCN	NATTACNCGC	T	TTCNTGAGTA	T	CACTCCCCCG	AATCTCACCC	TACTCAACTC	420
AAAAANATCN	GATACAAAAT	A	AATNCAAGCC	T	GNNTATNAC	ACTNTGACTG	GGTCTCTATT	480
TTAGNGGTCC	NTNAANCNTC	C	TAATACTTC	C	AGTCTNCCCT	TCNCCAATTT	CCNAANGGCT	540
CTTTCNGACA	GCAINTTTTG	G	TTTCCCNNTT	G	GGTTCCTTAN	NGAATTGCCC	TTCNTNGAAC	600
GGGCTCNTCT	TTTCCTTCGG	T	TANCTTGGN	T	TCNNCCGGC	CAGTTATTAT	TTCCCNNTTTT	660
AAATTCNTNC	CNTTTANTTT	T	TGCNTTCNA	A	AACCCCGGC	CTTGAAAACG	GCCCCCTGGT	720
AAAAGTTGT	TTTGANAAAA	T	TTTTTGTTTT	G	TTC			755

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 849 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTTTTTTTTT	TTTTTANGTG	TNGTCGTGCA	GGTAGAGGCT	TACTACAANT	GTGAANACGT	60
ACGCTNGGAN	TAANGCGACC	CGANTTCTAG	GANNCNCCCT	AAAATCANAC	TGTGAAGATN	120
ATCCTGNNNA	CGGAANGGTC	ACCGGNNGAT	NNTGCTAGGG	TGNCCNCTCC	CANNNCNTTN	180
CATAACTCNG	NGGCCCTGCC	CACCACCTTC	GGCGGCCCN	NGNCCGGGCC	CGGGTCATTN	240
GNNTTAACCN	CACTNNGCNA	NCGGTTTCN	NCCCCNCCNG	ACCCNGGCCA	TCCGGGGTNC	300
TCTGTCTTCC	CCTGNAGNCN	ANAAANTGGG	CCNCGNCCC	CTTTACCCCT	NNACAAGCCA	360
CNGCCNTCTA	NCCNCNGCCC	CCCCTCCANT	NNGGGGGACT	GCCNANNGCT	CCGTTNCTNG	420
NNACCCCN	GGGTNCCTCG	GTTGTCGANT	CNACCGNANG	CCANGGATTC	CNAAGGAAGG	480
TGCGTTNTTG	GGCCCTACCC	TTCGCTNCGG	NNCACCCCTC	CCGACNANGA	NCCGCTCCCCG	540
CNCNCGNNG	CCTCNCCTCG	CAACACCCGC	NCTCNTCNGT	NCGGNNNCCC	CCCCACCCGC	600
NCCCTCNCNC	NGNCGNANCN	CTCCNCCNCC	GTCTCANCA	CCACCCGCC	CCGCCAGGCC	660
NTCANCCACN	GGNNGACNNG	NAGCNCNNTC	GCNCCGCGCN	GCGNCCCT	CGCCNCNGAA	720
CTNCNTCNGG	CCANTNNGCG	TCAANCCNNA	CNAAACGCCG	CTGCGCGGCC	CGNAGCGNCC	780
NCCTCCNCGA	GTCTCCCGN	CTTCNACCC	ANGNNTTCN	CGAGGACACN	NNACCCGCC	840
NNCANGCGG						849

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCGCAAAC	TACTTCGCTC	GNACTCGTGC	GCCTCGCTNC	TCTTTTCCTC	CGCAACCATG	60
TCTGACNANC	CCGATTNNGC	NGATATCNAN	AAGNTCGANC	AGTCCAAACT	GANTAACACA	120
CACACNCNAN	AGANAAATCC	NCTGCCTTCC	ANAGTANACN	ATTGAACNNG	AGAACCANGC	180
NGGCGAATCG	TAATNAGGCG	TGCGCCGCCA	ATNTGTCNCC	GTTTATTNTN	CCAGCNTCNC	240
CTNCCNACCC	TACNTCTTCN	NAGCTGTCTN	ACCCCTNGTN	CGNACCCCCC	NAGGTCGGGA	300
TCGGGTTTNN	NNTGACCGNG	CNNCCCCCTC	CCCCNTCCAT	NACGANCCNC	CCGCACCACC	360
NANNGCNCGC	NCCCCGNCT	CTTCGCCNCC	CTGTCTTNTN	CCCCTGTNGC	CTGGCNCNGN	420
ACCGCATTGA	CCCTCGCCNN	CTNCNNGAAA	NCGNANACGT	CCGGGTTGNN	ANNANCGCTG	480
TGGGNNGCG	TCTGCNCCGC	GTTCTTCCN	NCNCTTCCA	CCATCTTCNT	TACNNGGTCT	540
CCNCGCCNTC	TCNNNCACNC	CCTGGGACGC	TNTCTNTG	CCCCCTTNAC	TCCCCCCTT	600
CGNCGTGNC	CGNCCCCACC	NTCATTNTCA	NACGNTCTTC	ACAANNNCCT	GGNTNNTCTC	660
CNANCNGNCN	GTACNCCNAG	GGAAGGNGG	GGNNCCNNTG	NTTGACGTTG	NGGNGANGTC	720
CGAANANTCC	TCNCCNTCAN	CNCTACCCCT	CGGGCGNNCT	CTCNGTTNCC	AACTTANCAA	780
NTCTCCCCCG	NGNGCNCNTC	TCAGCCTCNC	CCNCCCCNCT	CTCTGCANTG	TNCTCTGCTC	840
TNACCNTTAC	GANTNTTCGN	CNCCCTCTTT	CC			872

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCATGCAAGC	TTGAGTATTC	TATAGNGTCA	CCTAAATANC	TTGGCNTAAT	CATGGTCNTA	60
NCTGNCTTCC	TGTGTCAAAT	GTATACNAAN	TANATATGAA	TCTNATNTGA	CAAGANNGTA	120

TCNTNCATTA	GTAACAANTG	TNNTGTCCAT	CCTGTCNGAN	CANATTCCCA	TNNATTNCGN	180
CGCATTNCN	GCNCANTATN	TAATNGGGAA	NTCNNNTNNN	NCACCNNCAT	CTATCNTNCC	240
GCNCCCTGAC	TGGNAGAGAT	GGATNANTTC	TNNTNTGACC	NACATGTTCA	TCTTGGATTN	300
AANANCCCCC	CGCNGNCCAC	CGGT'TNGNNG	CNAGCCNNTC	CCAAGACCTC	CTGTGGAGGT	360
AACCTGCGTC	AGANNCATCA	AACNTGGGAA	ACCCGCNNCC	ANGTNNAAGT	NGNNNCANAN	420
GATCCCGTCC	AGGNTTNACC	ATCCCTTCNC	AGCGCCCCCT	TTNGTGCCTT	ANAGNGNAGC	480
GTGTCCNANC	CNCTCAACAT	GANACGCGCC	AGNCCANCCG	CAATTNGGCA	CAATGTGCGN	540
GAACCCCTTA	GGGGGANTNA	TNCAAANCCC	CAGGATTGTC	CNCNCANGAA	ATCCCNANC	600
CCCNCCCTAC	CCNCTTTGG	GACNGTGACC	AANTCCCGGA	GTNCCAGTCC	GGCCNGNCTC	660
CCCCACCGGT	NNCNTGGGG	GGGTGAANCT	CNGNNTCANC	CNGNCGAGGN	NTCGNAAGGA	720
ACCGGNCCTN	GGNCGAANNG	ANCNNTCNGA	AGNGCCNCNT	CGTATAACCC	CCCCCNCCA	780
NCCNACNGNT	AGNTCCCCC	CNGGGTNCGG	AANGG			815

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCGAGATGTC	TCGCTCCGTG	GCCTTAGCTG	TGCTCGCGCT	ACTCTCTCTT	TCTGGCCTGG	60
AGGCTATCCA	GCGTACTCCA	AAGATTACAG	TTTACTCACG	TCATCCAGCA	GAGAATGGAA	120
AGTCAAATTT	CCTGAATTGC	TATGTGTCTG	GGTTTCATCC	ATCCGACATT	GAANTTGACT	180
TACTGAAGAA	TGGANAGAGA	ATTGAAAAAG	TGGAGCATTG	AGACTTGTCT	TTCAGCAAGG	240
ACTGGTCTTT	CTATCTCNTG	TACTACACTG	AATTACCCCC	CACTGAAAAA	GATGAGTATG	300
CCTGCCGTGT	GAACCATGTG	ACTTTGTCTC	AGCCCCAAGAT	AGTTAAGTGG	GATCGAGACA	360
TGTAAGCAGN	CNNCATGGAA	GTTTGAAGAT	GCCGCATTTG	GATTGGATGA	ATTCCAAATT	420
CTGCTTGCTT	GCNTTTTAAT	ANTGATATGC	NTATACACCC	TACCCTTTAT	GNCCCCAAAT	480
TGTAGGGGTT	ACATNANTGT	TCNCNTNGGA	CATGATCTTC	CTTTATAANT	CCNCCNTTCG	540
AATTGCCCGT	CNCCCNNGTN	NGAATGTTTC	CNNAACCACG	GTTGGCTCCC	CCAGGTCNCC	600
TCTTACGGAA	GGGCCTGGGC	CNCTTTNCAA	GGTTGGGGGA	ACCNAAAATT	TCNCTTNTGC	660
CCNCCCNCCA	CNNTCTTGNG	NNCNCANTTT	GGAACCCCTC	CNATTCCCCCT	TGGCCTCNNA	720
NCCTTNNTCTA	ANAAAACTTN	AAANCGTNGC	NAAANNTTTN	ACTTCCCCC	TTACC	775

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ANATTANTAC	AGTGTAATCT	TTTCCCAGAG	GTGTGTANAG	GGAACGGGGC	CTAGAGGCAT	60
CCCANAGATA	NCTTATANCA	ACAGTGCTTT	GACCAAGAGC	TGCTGGGCAC	ATTTCTTGCA	120
GAAAAGGTGG	CGGTCCCCAT	CACCTCTCCT	CTCCCATAGC	CATCCCAGAG	GGGTGAGTAG	180
CCATCANGCC	TTCGGTGGGA	GGGAGTCANG	GAAACAACAN	ACCACAGAGC	ANACAGACCA	240
NTGATGACCA	TGGGCGGGAG	CGAGCCTCTT	CCCTGNACCG	GGGTGGCANA	NGANAGCCTA	300
NCTGAGGGGT	CACACTATAA	ACGTTAACGA	CCNAGATNAN	CACCTGCTTC	AAGTGCACCC	360
TTCTTACCTG	ACNACCAGNG	ACNNNNAACT	GCNGCCTGGG	GACAGCNCTG	GGANCAGCTA	420
ACNNAGCACT	CACCTGCCCC	CCCATGGCCG	TNCGCNTCCC	TGGTCCTGNC	AAGGGAAGCT	480
CCCTGTTGGA	ATTNCGGGGA	NACCAAGGGA	NCCCCCTCCT	CCANCTGTGA	AGGAAAAANN	540
GATGAATTT	TNCCCTTCCG	GCCNNTCCCC	TCTTCCTTTA	CACGCCCCCT	NNTACTCNTC	600

TCCCTCTNTT	NTCCTGNCNC	ACTTTTNACC	CCNNNATTTC	CCTTNATTGA	TCGGANNCTN	660
GANATTCCAC	TNNCGCCTNC	CNTCNATCNG	NAANACNAAA	NACTNTCTNA	CCNNGGGGAT	720
GGGNCCCTCG	NTCATCCTCT	CTTTTTCNCT	ACCNCNNNTT	CTTTGCCTCT	CCTTNGATCA	780
TCCAACNCTC	GNTGGCCNTN	CCCCCCCNNN	TCCTTTNCCC			820

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCTGGGTGAT	GGCCTCTTCC	TCCTCAGGGA	CCTCTGACTG	CTCTGGGCCA	AAGAATCTCT	60
TGTTTCTTCT	CCGAGCCCCA	GGCAGCGGTG	ATTGAGCCCT	GCCCAACCTG	ATTCTGATGA	120
CTGCGGATGC	TGTGACGGAC	CCAAGGGGCA	AATAGGGTCC	CAGGGTCCAG	GGAGGGGCGC	180
CTGCTGAGCA	CTTCCGCCCC	TCACCCTGCC	CAGCCCCTGC	CATGAGCTCT	GGGCTGGGTC	240
TCCGCCTCCA	GGGTTCTGCT	CTTCCANGCA	NGCCANCAAG	TGGCGCTGGG	CCACACTGGC	300
TTCTTCCTGC	CCCNTCCCTG	GCTCTGANTC	TCTGTCTTCC	TGTCCTGTGC	ANGCNCCTTG	360
GATCTCAGTT	TCCCTCNCCT	ANNGAACTCT	GTTTCTGANN	TCTTCANTTA	ACTNTGANTT	420
TATNACCANAN	TGGNCTGTNC	TGTCNNACTT	TAATGGGCCN	GACCGGCTAA	TCCCTCCCTC	480
NCTCCCTTCC	ANTTCNNNNA	ACCNGCTTNC	CNTCNTCTCC	CCNTANCCCG	CCNNGGAANC	540
CTCCTTTGCC	CTNACCANGG	GCCNNNACCG	CCCNNTNCTN	GGGGGGCNNG	GTNNCTNCNC	600
CTGNTNNCCC	CNCTCNCNNT	TNCCTCGTCC	CNNCNCNCGN	NNGCANNTTC	NCNGTCCCN	660
TNNCTCTTCN	NGTNTCGNAA	NGNTCNCNTN	TNNNNNGNCN	NGNTNNTNCN	TCCCTCTCNC	720
CNNNTGNANG	TNNTTNNNNC	NCNGNNCCCC	NNNNCNNNNN	NGGNNNTNNN	TCTNCNCNGC	780
CCCNCCCCC	NGNATTAAGG	CCTCCNNTCT	CCGGCCNC			818

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGAAGGGCG	GAGGGATATT	GTANGGGATT	GAGGGATAGG	AGNATAANGG	GGGAGGTGTG	60
TCCCAACATG	ANGGTGNNGT	TCTCTTTTGA	ANGAGGGTTG	NGTTTTTANN	CCNNGTGGGT	120
GATTNAAACC	CATTGTATGG	AGNNAAAGGN	TTTNAGGGAT	TTTTCGGGCTC	TTATCAGTAT	180
NTANATTCCCT	GTNAATCGGA	AAATNATNTT	TCNNCNGGAA	AATNTTGCTC	CCATCCGNAA	240
ATTNCTCCCG	GGTAGTGCA	NTTNGGGGGN	CNGCCANGTT	TCCCAGGCTG	CTANAATCGT	300
ACTAAAGNTT	NAAGTGGGAN	TNCAAATGAA	AACCTNNCAC	AGAGNATCCN	TACCCGACTG	360
TNNNTTNCCT	TCGCCCTNTG	ACTCTGCNNG	AGCCCAATAC	CCNNGNGNAT	GTNCCCNGN	420
NNNGCGNCNC	TGAAANNNNC	TCGNGGCTNN	GANCATCANG	GGGTTTCGCA	TCAAAAGCNC	480
CGTTTCNCAT	NAAGGCACTT	TNGCCTCATC	CAACCNTNG	CCCTCNCNCA	TTTNGCCGTC	540
NGGTTNCNCT	ACGCTNNTNG	CNCCTNNNTN	GANATTTTNC	CCGCCTNGGG	NAANCCTCCT	600
GNAATGGGTG	GGGNCCTTTC	TTTTNACCNN	GNGGTNTACT	AATCNCNTNC	ACGCNTNCTT	660
TCTCNACCCC	CCCCCTTTT	CAATCCCANC	GGCNAATGGG	GTCTCCCCNN	CGANGGGGGG	720
NNNCCCANN	C					731

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ACTAGTCCAG	TGTGGTGGAA	TTCCATTGTG	TTGGGGNCNC	TTCTATGANT	ANTNTTAGAT	60
CGCTCANACC	TCACANCTC	CCNACNANGC	CTATAANGAA	NANNAATAGA	NCTGTNCNNT	120
ATNTNTACNC	TCATANNCT	CNNNACCCAC	TCCCTCTTAA	CCCNTACTGT	GCCTATNGCN	180
TNNCTANTCT	NTGCCGCCTN	CNANCCACCN	GTGGGCCNAC	CNCNNGNATT	CTCNATCTCC	240
TCNCCATNTN	GCCTANANTA	NGTNCATACC	CTATACCTAC	NCCAATGCTA	NNNCTAANCN	300
TCCATNANTT	ANNNTAACTA	CCACTGACNT	NGACTTTTNC	ATNANCTCCT	AATTTGAATC	360
TACTCTGACT	CCCACNGCCT	ANNNATTAGC	ANCNTCCCCC	NACNATNTCT	CAACCAAATC	420
NTCAACAACC	TATCTANCTG	TTCNCCAACC	NTNCTCTCCG	ATCCCCNNAC	AACCCCCCTC	480
CCAAATACCC	NCCACCTGAC	NCCTAACCCN	CACCATCCCC	GCAAGCCNAN	GGNCATTAN	540
CCACTGGAAT	CACNATNGGA	NAAAAAAAC	CCNAACTCTC	TANCNCNNAT	CTCCCTAANA	600
AATNCTCCTN	NAATTTACTN	NCANTNCCAT	CAANCCCCACN	TGAAACNNAA	CCCCTGTTTT	660
TANATCCCTT	CTTTCGAAAA	CCNACCCCTT	ANNNCCCAAC	CTTNGGGGCC	CCCCCNCTNC	720
CCNAATGAAG	GNCNCCCAAT	CNANGAAACG	NCCNTGAAAA	ANCNAGGCNA	ANANNNTCCG	780
CANATCCTAT	CCCTTANTTN	GGGGNCCCTT	NCCNGGGGCC	CC		822

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 787 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGGCCGCCTG	CTCTGGCACA	TGCCTCCTGA	ATGGCATCAA	AAGTGATGGA	CTGCCCATTG	60
CTAGAGAAGA	CCTTCTCTCC	TACTGTCAAT	ATGGAGCCCT	GCAGACTGAG	GGCTCCCCCT	120
GTCTGCAGGA	TTTGATGTCT	GAAGTCGTGG	AGTGTGGCTT	GGAGCTCCTC	ATCTACATNA	180
GCTGGAAGCC	CTGGAGGGCC	TCTCTCGCCA	GCCTCCCCCT	TCTCTCCACG	CTCTCCANGG	240
ACACCAGGGG	CTCCAGGCAG	CCCATTATTC	CCAGNANGAC	ATGGTGTTTC	TCCACGCGGA	300
CCCATGGGGC	CTGNAAGGCC	AGGGTCTCCT	TTGACACCAT	CTCTCCCGTC	CTGCCTGGCA	360
GGCCGTGGGA	TCCACTANTT	CTANAACGGN	CGCCACCNCG	GTGGGAGCTC	CAGCTTTTGT	420
TCCNNTTAAT	GAAGGTTAAT	TGCNCGCTTG	GCGTAATCAT	NGGTCANAAC	TNTTTCCTGT	480
GTGAAATTGT	TTNTCCCCCT	NCNATTCCNC	NCNACATAACN	AACCCGGAAN	CATAAAGTGT	540
TAAAGCCTGG	GGGTNGCCTN	NNGAATNAAC	TNAACTCAAT	TAATTGCGTT	GGCTCATGGC	600
CCGCTTTCCN	TTCNGGAAAA	CTGTCNTCCC	CTGCNTTNNT	GAATCGGCCA	CCCCCNNGGG	660
AAAAGCGGTT	TGCNTTTTNG	GGGGNTCCTT	CCNCTTCCCC	CCTCNCTAAN	CCCTNCGCCT	720
CGGTCGTTNC	NGGTNGCGGG	GAANGGGNAT	NNNCTCCNC	NAAGGGGGNG	AGNNNGNTAT	780
CCCCAAA						787

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 799 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTTTTTTTT	TTTTTTTGGC	GATGCTACTG	TTTAATTGCA	GGAGGTGGGG	GTGTGTGTAC	60
CATGTACCAG	GGCTATTAGA	AGCAAGAAGG	AAGGAGGGAG	GGCAGAGCGC	CCTGCTGAGC	120
AACAAAGGAC	TCCTGCAGCC	TTCTCTGTCT	GTCTCTTGGC	GCAGGCACAT	GGGGAGGCCCT	180
CCCGCAGGGT	GGGGGCCACC	AGTCCAGGGG	TGGGAGCACT	ACANGGGGTG	GGAGTGGGTG	240
GTGGCTGGTN	CNAATGGCCT	GNCACANATC	CCTACGATTC	TTGACACCTG	GATTTCACCA	300
GGGGACCTTC	TGTTCTCCCA	NGGNAACTTC	NTNNATCTCN	AAAGAACACA	ACTGTTTCTT	360
CNGCANTTCT	GGCTGTTTAT	GGAAAGCACA	GGTGTCCTAT	TTNGGCTGGG	ACTTGGTACA	420
TATGGTTCCG	GCCCACCTCT	CCCNTCNAAN	AAGTAATCA	CCCCCCCCCN	CCNTCTNTTG	480
CCTGGGCCCT	TAANTACCCA	CACCGGAATC	CANTTANTTA	TTCATCTTNG	GNTGGGCTTG	540
NTNATCNCCN	CCTGAANGCG	CCAAGTTGAA	AGGCCACGCC	GTNCCCNCTC	CCCATAGNAN	600
NTTTTNNCNT	CANCTAATGC	CCCCCNGGC	AACNATCCAA	TCCCCCCCCN	TGGGGGCCCC	660
AGCCCANGGC	CCCCGNCTCG	GGNNNCCNGN	CNCGNANTCC	CCAGGNTCTC	CCANTCNGNC	720
CCNNNGCNCC	CCCGCACGCA	GAACANAAGG	NTNGAGCCNC	CGCANNNNNN	NGGTNNCNAC	780
CTCGCCCCCC	CCNCGNNG					799

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
TTTTNCCNAG	GGCAGGTTTA	TTGACAACCT	CNCGGGACAC	AANCAGGCTG	GGGACAGGAC	120
GGCAACAGGC	TCCGGCGGCG	GCGGCGGCGG	CCCTACCTGC	GGTACCAAAT	NTGCAGCCTC	180
CGCTCCCGCT	TGATNTTCCT	CTGCAGCTGC	AGGATGCCNT	AAAACAGGGC	CTCGGCCNTN	240
GGTGGGCACC	CTGGGATTNN	AATTTCCACG	GGCACAATGC	GGTCGCANCC	CCTCACCACC	300
NATTAGGAAT	AGTGGTNTTA	CCNCCNCCG	TTGGCNCAC	CCCCNTGGAA	ACCACTTNTC	360
GCGGCTCCGG	CATCTGGTCT	TAAACCTTGC	AAACNCTGGG	GCCCTCTTTT	TGGTTANTNT	420
NCCNGCCACA	ATCATNACTC	AGACTGGCNC	GGGCTGGCCC	CAAAAAANCN	CCCCAAAACC	480
GGNCCATGTC	TTNNCGGGGT	TGCTGCNATN	TNCATCACCT	CCCGGGCNCA	NCAGGNCAAC	540
CCAAAAGTTC	TTNGGGCCCN	CAAAAAANCT	CCGGGGGGNC	CCAGTTTCAA	CAAAGTCATC	600
CCCCTTGGCC	CCCAAATCCT	CCCCCGGNTT	NCTGGGTTTG	GGAACCCACG	CCTCTNNCTT	660
TGGNNGGCAA	GNTGGNTCCC	CCTTCGGGCC	CCCGGTGGGC	CCNNCTCTAA	NGAAAACNCC	720
NTCCTNNNCA	CCATCCCCCC	NNGNNACGNC	TANCAANGNA	TCCCTTTTTT	TANAAACGGG	780
CCCCCNCNG						789

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GACAGAACAT	GTTGGATGGT	GGAGCACCTT	TCTATACGAC	TTACAGGACA	GCAGATGGGG	60
AATTCATGGC	TGTTGGAGCA	ATANAACCCC	AGTTCTACGA	GCTGCTGATC	AAAGGACTTG	120
GACTAAAGTC	TGATGAACTT	CCCAATCAGA	TGAGCATGGA	TGATTGGCCA	GAAATGAANA	180
AGAAGTTTGC	AGATGTATTT	GCAAAGAAGA	CGAAGGCAGA	GTGGTGTCAA	ATCTTTGACG	240
GCACAGATGC	CTGTGTGACT	CCGTTTCTGA	CTTTTGAGGA	GGTTGTTTAT	CATGATCACA	300

ACAANGAACG	GGGCTCGTTT	ATCACCANTG	AGGAGCAGGA	CGTGAGCCCC	CGCCCTGCAC	360
CTCTGCTGTT	AAACACCCCA	GCCATCCCTT	CTTTCAAAAG	GGATCCACTA	CTTCTAGAGC	420
GGNCGCCACC	GCGGTGGAGC	TCCAGCTTTT	GTTCCCTTTA	GTGAGGGTTA	ATTGCCGCGT	480
TGGCGTAATC	ATGGTCATAN	CTGTTCCTG	TGTGAAATTG	TTATCCGCTC	ACAATTCCAC	540
ACAACATACG	ANCCGGAAGC	ATNAAATTTT	AAAGCCTGGN	GGTNGCCTAA	TGANTGAACT	600
NACTCACATT	AATTGGCTTT	GCGCTCACTG	CCCGCTTTCC	AGTCCGGAAA	ACCTGTCCTT	660
GCCAGCTGCC	NTTAATGAAT	CNCGCCACCC	CCCGGGGAAA	AGGCNGTTTG	CTTNTTGGGG	720
CGCNCTTCCC	GCTTTCTCGC	TTCCTGAANT	CCTTCCCCCC	GGTCTTTCGG	CTTGCGGCNA	780
ACGGTATCNA	CCT					793

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCCGCGACCG	GCATGTACGA	GCAACTCAAG	GGCGAGTGGA	ACCGTAAAAG	CCCCAATCTT	60
ANCAAGTGCG	GGGAANAGCT	GGGTCGACTC	AAGCTAGTTC	TTCTGGAGCT	CAACTTCTTG	120
CCAACCACAG	GGACCAAGCT	GACCAAACAG	CAGCTAATTC	TGGCCCGTGA	CATACTGGAG	180
ATCGGGGCCC	AATGGAGCAT	CCTACGCAAN	GACATCCCTT	CCTTCGAGCG	CTACATGGCC	240
CAGCTCAAAT	GCTACTACTT	TGATTACAAN	GAGCAGCTCC	CCGAGTCAGC	CTATATGCAC	300
CAGCTCTTGG	GCCTCAACCT	CCTCTTCCTG	CTGTCCCAGA	ACCGGGTGGC	TGANTNCCAC	360
ACGGANTTGG	ANCGGCTGCC	TGCCCAANGA	CATACANACC	AATGTCTACA	TCNACCACCA	420
GTGTCTTGGA	GCAATACTGA	TGGANGGCAG	CTACCNCAA	GTNTTCCTGG	CCNAGGGTAA	480
CATCCCCCGC	CGAGAGCTAC	ACCTTCTTCA	TTGACATCCT	GCTCGACACT	ATCAGGGATG	540
AAAATCGCNG	GGTTGCTCCA	GAAAGGCTNC	AANAANATCC	TTTCNCTGA	AGGCCCCCGG	600
ATNCNCTAGT	NCTAGAAATG	GCCCGCCATC	GCGGTGGANC	CTCCAACCTT	TCGTTNCCCT	660
TTACTGAGGG	TTNATTGCCG	CCCTTGCGGT	TATCATGGTC	ACNCCNGTTN	CCTGTGTGTA	720
AATTNTTAAC	CCCCACAAT	TCCACGCCNA	CATTNG			756

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGGGATCTCT	ANATCNACCT	GNATGCATGG	TGTGCGGTGT	GGTCGCTGTC	GATGAANATG	60
AACAGGATCT	TGCCCTTGAA	GCTCTCGGCT	GCTGTNTTTA	AGTTGCTCAG	TCTGCCGTCA	120
TAGTCAGACA	CNCTCTTGGG	CAAAAAACAN	CAGGATNTGA	GTCTTGATTT	CACCTCCAAT	180
AATCTTCNGG	GCTGTCTGCT	CGGTGAACTC	GATGACNANG	GGCAGCTGGT	TGTGTNTGAT	240
AAANTCCANC	ANGTTCTCCT	TGGTGACCTC	CCCTTCAAAG	TTGTTCCGGC	CTTCATCAAA	300
CTTCTNNAAN	ANGANNANCC	CANCTTTGTC	GAGCTGGNAT	TTGGANAACA	CGTCACTGTT	360
GGAAACTGAT	CCCAAATGGT	ATGTCATCCA	TGCCTCTGTC	TGCCTGCAAA	AAACTTGCTT	420
GGCNCAAATC	CGACTCCCN	TCCTTGAAAG	AAGCCNATCA	CACCCCCCTC	CCTGGACTCC	480
NNCAANGACT	CTNCCGCTNC	CCCNTCCNNG	CAGGGTTGGT	GGCANNCCGG	GCCCNTGCGC	540
TTCTTCAGCC	AGTTCAACAT	NTTCATCAGC	CCCTCTGCCA	GCTGTNTAT	TCCTTGGGGG	600
GGAAANCCGT	TCTCCCTTCC	TGAANNAACT	TTGACCGTNG	GAATAGCCGC	GCNTCNCCNT	660
ACNTNCTGGG	CCGGGTTCAA	ANTCCCTCCN	TTGNCNNTCN	CCTCGGGCCA	TTCTGGATTT	720
NCCNAACTTT	TTCCTTCCCC	CNCCCNCCGG	NGTTTGGNTT	TTTCATNGGG	CCCCAACTCT	780

GCTNTTGGCC ANTCCCCTGG GGGCNTNTAN CNCCCCCTNT GGTCCCNTNG GGCC

834

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 814 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGGNCGCTTT	CCNGCCGCGC	CCCGTTTCCA	TGACNAAGGC	TCCCTTCANG	TTAAATACNN	60
CCTAGNAAAC	ATTAATGGGT	TGCTCTACTA	ATACATCATA	CNAACCAGTA	AGCCTGCCCA	120
NAACGCCAAC	TCAGGCCATT	CCTACCAAAG	GAAGAAAGGC	TGGTCTCTCC	ACCCCTGTGA	180
GGAAAGGCCT	GCCTTGTAAG	ACACCACAAT	NCGGCTGAAT	CTNAAGTCTT	GTGTTTTACT	240
AATGGAAAAA	AAAAATAAAC	AANAGGTTTT	GTTCTCATGG	CTGCCCACCG	CAGCCTGGCA	300
CTAAACANC	CCAGCGCTCA	CTTCTGCTTG	GANAAATATT	CTTTGCTCTT	TTGGACATCA	360
GGCTTGATGG	TATCACTGCC	ACNTTTCAC	CCAGCTGGGC	NCCCTTCCCC	CATNTTGTG	420
ANTGANCTGG	AAGGCCTGAA	NCTTAGTCTC	CAAAAGTCTC	NGCCCACAAG	ACCGGCCACC	480
AGGGGANGTC	NTTINCAGTG	GATCTGCCAA	ANANTACCCN	TATCATCNNT	GAATAAAAAG	540
GCCCCTGAAC	GANATGCTTC	CANCANCTT	TAAGACCCAT	AATCCTNGAA	CCATGGTGCC	600
CTTCCGTCT	GATCCNAAAG	GAATGTTCT	GGGTCCANT	CCCTCCTTTG	TTNCTTACGT	660
TGTNTTGGAC	CCNTGCTNGN	ATNACCCAAN	TGANATCCCC	NGAAGCACCC	TNCCCCTGGC	720
ATTTGANTTT	CNTAAATTCT	CTGCCCTACN	NCTGAAAGCA	CNATTCCCTN	GGCNCCNAAN	780
GGNGAACTCA	AGAAGGTCTN	NGAAAAACCA	CNCN			814

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 760 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCATGCTGCT	CTTCCTCAAA	GTTGTTCTTG	TGCCATAAC	AACCACCATA	GGTAAAGCGG	60
GCGCAGTGTT	CGCTGAAGGG	GTTGTAGTAC	CAGCGCGGGA	TGCTCTCCTT	GCAGAGTCCT	120
GTGTCTGGCA	GGTCCACGCA	ATGCCCTTTG	TCACTGGGGA	AATGGATGCG	CTGGAGCTCG	180
TCNAANCCAC	TCGTGTATTT	TTACANGCA	GCCTCCTCCG	AAGCNTCCGG	GCAGTTGGGG	240
GTGTCGTAC	ACTCCACTAA	ACTGTGATN	CANCAGCCCA	TTGCTGCAGC	GGAAGTGGGT	300
GGGCTGACAG	GTGCCAGAAC	ACACTGGATN	GGCCTTTCCA	TGGAAGGGCC	TGGGGGAAAT	360
CNCCTNANCC	CAAACTGCCT	CTCAAAGGCC	ACCTTGACCA	CCCCGACAGG	CTAGAAATGC	420
ACTCTTCTTC	CCAAAGGTAG	TTGTTCTTGT	TGCCCAAGCA	NCCTCCANCA	AACCAAAANC	480
TTGCAAAATC	TGCTCCGTGG	GGGTCAATNN	TACCANGGTT	GGGGAAANAA	ACCGGCGNGN	540
GANCCNCCTT	GTTTGAATGC	NAAGGNAATA	ATCCTCCTGT	CTTGCTTGGG	TGGAANAGCA	600
CAATTGAACT	GTTAACNTTG	GGCCGNGTTC	CNCTNGGGTG	GTCTGAAACT	AATCACCCTC	660
ACTGGAAAAA	GGTANGTGCC	TTCTTGAAT	TCCCAAANTT	CCCCTNGNTT	TGGGTNNTTT	720
CTCTCTNCC	CTAAAAATCG	TNTTCCCCC	CCNTANGGCG			760

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 724 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTAAAAA CCCCCTCCAT TGAATGAAAA    60
CTTCCNAAAT TGTCCAACCC CCTCNNCCAA ATNNCCATTT CCGGGGGGGG GTTCCAAACC    120
CAAATTAATT TTGGANTTTA AATTAAATNT TNATTNGGGG AANAANCCAA ATGTNAAGAA    180
AATTTAACCC ATTATNAACT TAAATNCCTN GAAACCCNTG GNTTCCAAAA ATTTTTAACC    240
CTTAAATCCC TCCGAAATTG NTAANGGAAA ACCAAATTCN CCTAAGGCTN TTTGAAGGTT    300
NGATTTAAAC CCCCTTNANT TTTTTTNACC CNNGNCTNAA NTATTTNGNT TCCGGTGTTT    360
TCCTNTTAAN CNTNGGTAAC TCCCGNTAAT GAANNCCCT AANCCAATTA AACCGAATTT    420
TTTTTGAATT GGAAATTCCN NGGGAATTNA CCGGGGTTTT TCCCNTTTGG GGGCCATNCC    480
CCCNCTTTCC GGGTTTGGGN NTAGGTTGAA TTTTNNANG NCCCCAAAAA NCCCCAANA    540
AAAAAATCC CAAGNNTTAA TTNGAATNTC CCCCTCCCA GGCCTTTTGG GAAAGGNGGG    600
TTTNTGGGGG CCNGGGANTT CNTTCCCCCN TTNCNCCCC CCCCCCNGGT AAANGGTTAT    660
NGNNTTTGGT TTTTGGGCC CTTNANGGAC CTTCCGATN GAAATTAAAT CCCC GGNGC    720
GCCG                                     724

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(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

TTTTTTTTTT TTTTCTTTG CTCACATTTA ATTTTATTT TGATTTTTTT TAATGCTGCA    60
CAACACAATA TTTATTTTCT TGTCTCTTT TATTTTCTTT TATTTGTTTG CTGCTGCTGT    120
TTTATTTTATT TTTACTGAAA GTGAGAGGGA ACTTTTGTGG CCTTTTTTCC TTTTCTGTA    180
GGCCGCCTTA AGCTTTCTAA ATTTGGAACA TCTAAGCAAG CTGAANGGAA AAGGGGGTTT    240
CGCAAAATCA CTCGGGGGAA NGGAAAGGTT GCTTTGTTAA TCATGCCCTA TGGTGGGTGA    300
TTAACTGCTT GTACAATTAC NTTTCACCTT TAATTAATTG TGCTNAANGC TTTAATTANA    360
CTTGGGGGTT CCTTCCCAN ACCAACCCCN CTGACAAAAA GTGCCNGCCC TCAAATNATG    420
TCCCGGCNNT CNTTGAAACA CACNGCNGAA NGTCTCTATT NTCCCNCCNC CAGGTNAAAA    480
TGAAGGGTTA CCATNTTTAA NCCACCTCC ACNTGGCNNN GCCTGAATCC TCNAAAANCN    540
CCTCAANCN AATTNCTNNG CCCCAGTCNC GCNTNNGTCC CNCCGGGCT CCGGGAANTN    600
CACCCCNCA ANNCNNTNNC NAACNAAAT CCGAAAATAT TCCCNNTCNC TCAATTCCTC    660
CNNAGACTNT CCTCNNCNAN CNCAATTTT TTTTNTTCAC GAACNCGNNC CNNAATGN    720
NNNNCNCCTC CNTNGTCCN NAATCNCCAN C                                     751

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(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

GTGGTATTTT CTGTAAGATC AGGTGTTTCT CCCTCGTAGG TTAGAGGAA ACACCTCAT    60
AGATGAAAAC CCCCCGAGA CAGCAGCACT GCAACTGCCA AGCAGCCGGG GTAGGAGGGG    120
CGCCCTATGC ACAGCTGGGC CCTTGAGACA GCAGGGCTTC GATGTCAGGC TCGATGTCAA    180

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TGGTCTGGAA	GCGGCGGCTG	TACCTGCGTA	GGGGCACACC	GTCAGGGGCC	ACCAGGAACT	240
TCTCAAAGTT	CCAGGCAACN	TCGTTGCGAC	ACACCGGAGA	CCAGGTGATN	AGCTTGGGGT	300
CGGTCATAAN	CGCGGTGGCG	TCGTGCTGG	GAGCTGGCAG	GGCCTCCCGC	AGGAAGGCNA	360
ATAAAAGGTG	CGCCCCGCA	CGTTCANCT	CGCACTTCTC	NAANACCATG	ANGTTGGGCT	420
CNAACCCACC	ACCANNCCGG	ACTTCCTTGA	NGGAATTCCC	AAATCTCTTC	GNTCTTGGGC	480
TTCTNCTGAT	GCCCTANCTG	GTTGCCCNEN	ATGCCAANCA	NCCCCAANCC	CCGGGGTCCCT	540
AAANCACCCN	CCTCCTCNTT	TCATCTGGGT	TNTTNTCCCC	GGACCNTGGT	TCCTCTCAAG	600
GGANCCCAT	TCTCNACCAN	TACTCACCNT	NCCCCCCNT	GNNACCCANC	CTTCTANNNG	660
TTCCCNCCCG	NCCTCTGGCC	CNTCAAANAN	GCTTNCACNA	CCTGGGTCTG	CCTTCCCCCC	720
TNCCCTATCT	GNACCCCNEN	TTTGTCTCAN	TNT			753

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACTATATCCA	TCACAACAGA	CATGCTTCAT	CCCATAGACT	TCTTGACATA	GCTTCAAATG	60
AGTGAACCCA	TCCTTGATT	ATATACATAT	ATGTTCTCAG	TATTTTGGGA	GCCTTTCCAC	120
TTCTTTAAAC	CTTGTTCAAT	ATGAACACTG	AAAATAGGAA	TTTGTGAAGA	GTTAAAAAGT	180
TATAGCTTGT	TTACGTAGTA	AGTTTTTGAA	GTCTACATTC	AATCCAGACA	CTTAGTTGAG	240
TGTTAAACTG	TGATTTTAA	AAAATATCAT	TTGAGAATAT	TCTTTCAGAG	GTATTTTCAT	300
TTTTACTTTT	TGATTAAATTG	TGTTTTATAT	ATTAGGGTAG	T		341

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACTTACTGAA	TTTAGTTCTG	TGCTCTTCCT	TATTTAGTGT	TGTATCATAA	ATACTTTGAT	60
GTTTCAAACA	TTCTAAATAA	ATAATTTTCA	GTGGCTTCAT	A		101

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACATCTTTGT TACAGTCTAA GATGTGTTCT TAAATCACCA TTCCTTCCTG GTCCTCACCC	60
TCCAGGGTGG TCTCACACTG TAATTAGAGC TATTGAGGAG TCTTTACAGC AAATTAAGAT	120
TCAGATGCCT TGCTAAGTCT AGAGTTCTAG AGTTATGTTT CAGAAAGTCT AAGAAACCCA	180
CCTCTTGAGA GGTCACTAAA GAGGACTTAA TATTTTCATAT CTACAAAATG ACCACAGGAT	240
TGGATACAGA ACGAGAGTTA TCCTGGATAA CTCAGAGCTG AGTACCTGCC CGGGGGCCGC	300
TCGAA	305

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACATAAATAT CAGAGAAAAG TAGTCTTTGA AATATTTACG TCCAGGAGTT CTTTGTCTTCT	60
GATTATTTGG TGTGTGTTTT GGTGTGTGTC CAAAGTATTG GCAGCTTCAG TTTTCATTTT	120
CTCTCCATCC TCGGGCATTG TTCCCAAATT TATATACCAG TCTTCGTCCA TCCACACGCT	180
CCAGAATTTT TCTTTGTAG TAATATCTCA TAGCTCGGCT GAGCTTTTCA TAGGTCATGC	240
TGCTGTTGTT CTCTTTTTTA CCCCATAGCT GAGCCACTGC CTCTGATTTT AAGAACCTGA	300
AGACGCCCTC AGATCGGTCT TCCCATTFTA TTAATCCTGG GTTCTTGTCT GGGTTCAAGA	360
GGATGTCGCG GATGAATTCC CATAAGTGAG TCCCTCTCGG GTTGTGCTTT TTGGTGTGGC	420
ACTTGGCAGG GGGGTCTTGC TCCTTTTCA TATCAGGTGA CTCTGCAACA GGAAGGTGAC	480
TGGTGGTTGT CATGGAGATC TGAGCCCGGC AGAAAGTTTT GCTGTCCAAC AAATCTACTG	540
TGCTACCATA GTTGGTGTC TATAAATAGT TCTNGTCTTT CCAGGTGTTC ATGATGGAAG	600
GCTCAGTTTG TTCAGTCTTG ACAATGACAT TGTGTGTGGA CTGGAACAGG TCACTACTGC	660
ACTGGCCGTT CCACTTCAGA TGCTGCAAGT TGCTGTAGAG GAGNTGCCCC GCCGTCCCTG	720
CCGCCCCGGT GAACTCCTGC AAACATCATG TGCAAAGGTG CTCGCCGTTG ATGTGGAAGT	780
CNTGGAAAGG GATACAATTG GCATCCAGCT GGTGTTGTGTC CAGGAGGTGA TGGAGCCACT	840
CCCACACCTG GT	852

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACAACAGACC CTTGCTCGCT AACGACCTCA TGCTCATCAA GTTGGACGAA TCCGTGTCCG	60
AGTCTGACAC CATCCGGAGC ATCAGCATTG CTTGCGAGTG CCCTACCGCG GGGAACTCTT	120
GCCTCGTTTC TGGCTGGGGT CTGCTGGCGA ACGGCAGAAT GCCTACCGTG CTGCACTGCG	180

TGAACGTGTC GGTGGTGTCT GAGGAGGTCT GCAGTAAGCT CTATGACCCG CTGT

234

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACTTTTTATT TAAATGTTA TAAGGCAGAT CTATGAGAAT GATAGAAAAC ATGGTGTGTA	60
ATTGATAGC AATATTTTGG AGATTACAGA GTTTTAGTAA TTACCAATTA CACAGTTAAA	120
AAGAAGATAA TATATTCCAA GCANATACAA AATATCTAAT GAAAGATCAA GGCAGGAAAA	180
TGANTATAAC TAATTGACAA TGGAAAATCA ATTTTAATGT GAATTGCACA TTATCCTTTA	240
AAAGCTTTCA AAANAAANAA TTATTGCAGT CTANTTAATT CAAACAGTGT TAAATGGTAT	300
CAGGATAAAN AACTGAAGGG CANAAAGAAT TAATTTTCAC TTCATGTAAC NCACCCANAT	360
TTACAATGGC TTAAATGCAN GGAAAAAGCA GTGGAAGTAG GGAAGTANTC AAGGTCTTTC	420
TGGTCTCTAA TCTGCCCTTAC TCTTTGGGTG TGGCTTTGAT CCTCTGGAGA CAGCTGCCAG	480
GGCTCCTGTT ATATCCACAA TCCCAGCAGC AAGATGAAGG GATGAAAAAG GACACATGCT	540
GCCTTCCTTT GAGGAGACTT CATCTCACTG GCCAACACTC AGTCACATGT	590

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACAAGGGGGC ATAATGAAGG AGTGGGGANA GATTTTAAAG AAGGAAAAAA AACGAGGCCC	60
TGAACAGAAT TTCTCTGNAC AACGGGGCTT CAAAATAATT TTCTTGGGGA GGTTCAGAC	120
GCTTCACTGC TTGAAACTTA AATGGATGTG GGACANAATT TTCTGTAATG ACCCTGAGGG	180
CATTACAGAC GGGACTCTGG GAGGAAGGAT AAACAGAAAG GGGACAAAGG CTAATCCCAA	240
AACATCAAAG AAAGGAAGGT GGCGTCATAC CTCCCAGCCT ACACAGTTCT CCAGGGCTCT	300
CCTCATCCCT GGAGGACGAC AGTGGAGGAA CAACTGACCA TGTCCCCAGG CTCCTGTGTG	360
CTGGCTCCTG GTCTTCAGCC CCCAGCTCTG GAAGCCCACC CTCTGCTGAT CTGCGTGGC	420
CCACACTCCT TGAACACACA TCCCAGGTT ATATTCTTGG ACATGGCTGA ACCTCCTATT	480
CCTACTTCCG AGATGCCTTG CTCCCTGCAG CCTGTCAAAA TCCCCTCAC CCTCCAAACC	540
ACGGCATGGG AAGCCTTTCT GACTTGCCTG ATTACTCCAG CATCTTGGA CAATCCCTGA	600
TTCCCCACTC CTTAGAGGCA AGATAGGGTG GTTAAGAGTA GGGCTGGACC ACTTGGAGCC	660
AGGCTGCTGG CTTCAAATTN TGGCTCATTT ACGAGCTATG GGACCTGGG CAAGTNATCT	720
TCACTTCTAT GGGCNTCATT TTGTTCTACC TGCAAAATGG GGGATAATAA TAGT	774

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```
CANAAATTGA AATTTTATAA AAAGGCATTT TTCTCTTATA TCCATAAAAT GATATAATTT    60
TTGCAANTAT ANAAATGTGT CATAAATTAT AATGTTTCCTT AATTACAGCT CAACGCAACT    120
TGGT                                124
```

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```
GCCGATGCTA CTATTTTATT GCAGGAGGTG GGGGTGTTT TATTATTCTC TCAACAGCTT    60
TGTGGCTACA GGTGGTGTCT GACTGCATNA AAAANTTTT TACGGGTGAT TGCAAAAATT    120
TTAGGGCACC CATATCCCAA GCANTGT                                147
```

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```
ACATTAAATT AATAAAAGGA CTGTTGGGGT TCTGCTAAAA CACATGGCTT GATATATTGC    60
ATGGTTTGAG GTTAGGAGGA GTTAGGCATA TGTTTTGGA GAGGGGT                107
```

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTCCTAGGAA GTCTAGGGGA CACACGACTC TGGGGTCACG GGGCCGACAC ACTTGCACGG	60
CGGGAAGGAA AGGCAGAGAA GTGACACCGT CAGGGGGAAA TGACAGAAAG GAAAATCAAG	120
GCCTTGCAAG GTCAGAAAGG GGAATCAGGG CTTCCACCAC AGCCCTGCCC CACTTGGCCA	180
CCTCCCTTTT GGGACCAGCA ATGT	204

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ACAAAGATAA CATTTATCTT ATAACAAAAA TTTGATAGTT TTAAAGGTTA GTATTGTGTA	60
GGGTATTTTC CAAAAGACTA AAGAGATAAC TCAGGTAAAA AGTTAGAAAT GTATAAAACA	120
CCATCAGACA GGTTTTTTAAA AAACAACATA TTACAAAATT AGACAATCAT CCTTAAAAAA	180
AAAACCTTCTT GTATCAATTT CTTTGTTC AATGACTGA CTTAANTATT TTAAATATT	240
TCANAAACAC TTCCTCAAAA ATTTTCAANA TGGTAGCTTT CANATGTNCC CTCAGTCCCA	300
ATGTTGCTCA GATAAATAAA TCTCGTGAGA ACTTACCACC CACCACAAGC TTTCTGGGGC	360
ATGCAACAGT GTCTTTTCTT TNCTTTTCT TTTTTTTTT TTACAGGCAC AGAAACTCAT	420
CAATTTTATT TGGATAACAA AGGGTCTCCA AATTATATTG AAAAATAAAT CCAAGTTAAT	480
ATCACTCTTG T	491

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACATAATTTA GCAGGGCTAA TTACCATAAG ATGCTATTTA TTAANAGGTN TATGATCTGA	60
GTATTAACAG TTGCTGAAGT TTGGTATTTT TATGCAGCAT TTTCTTTTGT CTTTGATAAC	120
ACTACAGAAC CCTTAAGGAC ACTGAAAATT AGTAAGTAAA GTTCAGAAAC ATTAGCTGCT	180
CAATCAAATC TCTACATAAC ACTATAGTAA TTAACACGTT AAAAAAAGT GTTGAAATCT	240
GCACTAGTAT ANACCGCTCC TGTCAGGATA ANACTGCTTT GGAACAGAAA GGGAAAAANC	300
AGCTTTGANT TTCTTTGTGC TGATANGAGG AAAGGCTGAA TTACCTTGTT GCCTCTCCCT	360
AATGATTGGC AGGTCNGGTA AATNCCAAAA CATATTCCAA CTCAACACTT CTTTTCNCNG	420
TANCTTGANT CTGTGTATTC CAGGANCAGG CGGATGGAAT GGGCCAGCCC NCGGATGTTC	480
CANT	484

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACTAAACCTC GTGCTTGTGA ACTCCATACA GAAAACGGTG CCATCCCTGA ACACGGCTGG	60
CCACTGGGTA TACTGCTGAC AACCGCAACA ACAAAAACAC AAATCCTTGG CACTGGCTAG	120
TCTATGTCCT CTCAAGTGCC TTTTGTGTTG T	151

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ACCTGGCTTG TCTCCGGGTG GTTCCCGGCG CCCCCACGG TCCCCAGAAC GGACACTTTC	60
GCCCTCCAGT GGATACTCGA GCCAAAGTGG T	91

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCGGATGTG CGTTGGTTAT ATACAAATAT GTCATTTTAT GTAAGGGACT TGAGTATACT	60
TGGATTTTTG GTATCTGTGG GTTGGGGGGA CGGTCCAGGA ACCAATACCC CATGGATACC	120
AAGGGACAAC TGT	133

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ACTCTGGAGA ACCTGAGCCG CTGCTCCGCC TCTGGGATGA GGTGATGCAN GCNGTGGCGC	60
GACTGGGAGC TGAGCCCTTC CCTTTGCGCC TGCCTCAGAG GATTGTTGCC GACNTGCANA	120
TCTCANTGGG CTGGATNCAT GCAGGGT	147

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACAGGGATAT AGGTTTNAAG TTATTGTNAT TGTAAAATAC ATTGAATTTT CTGTATACTC	60
TGATTACATA CATTTATCCT TAAAAAAGA TGTAAATCTT AATTTTATG CCATCTATTA	120
ATTTACCAAT GAGTTACCTT GTAAATGAGA AGTCATGATA GCACTGAATT TTAAC TAGTT	180
TTGACTTCTA AGTTTGGT	198

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACAACAAATG GGTGTGAGG AAGTCTTATC AGCAAACTG GTGATGGCTA CTGAAAAGAT	60
CCATTGAAAA TTATCATTAA TGATTTTAAA TGACAACTTA TCAAAAATC ACTCAATTTT	120
CACCTGTGCT AGCTTGCTAA AATGGGAGTT AACTCTAGAG CAAATATAGT ATCTTCTGAA	180
TACAGTCAAT AAATGACAAA GCCAGGGCCT ACAGGTGGTT TCCAGACTTT CCAGACCCAG	240
CAGAAGGAAT CTATTTTATC ACATGGATCT CCGTCTGTGC TCAAAATACC TAATGATATT	300
TTTCGTCTTT ATTGGACTTC TTTGAAGAGT	330

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ACCGTGGGTG CCTTCTACAT TCCTGACGGC TCCTTCACCA ACATCTGGTT CTACTTCGGC	60
GTCGTGGGCT CCTTCCTCTT CATCCTCATC CAGCTGGTGC TGCTCATCGA CTTTGCGCAC	120
TCCTGGAACC AGCGGTGGCT GGGCAAGGCC GAGGAGTGCG ATTCCCGTGC CTGGT	175

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ACCCCACTTT TCCTCCTGTG AGCAGTCTGG ACTTCTCACT GCTACATGAT GAGGGTGAGT	60
GTTTGTGCT CTTCAACAGT ATCCTCCCTT TTCCGGATCT GCTGAGCCGG ACAGCAGTGC	120
TGGACTGCAC AGCCCCGGGG CTCCACATTG CTGT	154

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGCTCGAGCC CTATAGTGAG TCGTATTAGA	30
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(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACAAGTCATT TCAGCACCCT TTGCTCTTCA AAAGTACCA TCTTTTATAT TTAATGCTTC	60
CTGTATGAAT AAAAATGGTT ATGTCAAGT	89

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACCGGAGTAA CTGAGTCGGG ACGCTGAATC TGAATCCACC AATAAATAAA GGTTCCTGCAG	60
AATCAGTGCA TCCAGGATTG GTCCTTGAT CTGGGGT	97

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ACAACAANAA NTCCCTTCTT TAGGCCACTG ATGGAAACCT GGAACCCCT TTGATGGCA	60
GCATGGCGTC CTAGGCCTTG ACACAGCGGC TGGGTTTGG GCTNTCCCAA ACCGCACACC	120
CCAACCCTGG TCTACCCACA NTTCTGGCTA TGGGCTGTCT CTGCCACTGA ACATCAGGGT	180
TCGGTCATAA NATGAAATCC CAANGGGGAC AGAGGTCAGT AGAGGAAGCT CAATGAGAAA	240
GGTGCTGTTT GCTCAGCCAG AAAACAGCTG CCTGGCATTG GCCGCTGAAC TATGAACCCG	300
TGGGGGTGAA CTACCCCAN GAGGAATCAT GCCTGGGCGA TGCAANGGTG CCAACAGGAG	360
GGGCGGGAGG AGCATGT	377

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACGCCTTTCC CTCAGAATTC AGGGAAGAGA CTGTGCCTCG CCTTCCTCCG TTGTTGCGTG	60
AGAACCCGTG TGCCCCCTCC CACCATATCC ACCCTCGCTC CATCTTTGAA CTCAAACACG	120
AGGAACTAAC TGCACCCTGG TCCTCTCCCC AGTCCCCAGT TCACCCTCCA TCCCTCACCT	180
TCCTCCACTC TAAGGGATAT CAACACTGCC CAGCACAGGG GCCCTGAATT TATGTGGTTT	240
TTATATATTT TTTAATAAGA TGCACCTTAT GTCATTTTTT AATAAAGTCT GAAGAATTAC	300
TGTTT	305

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACTACACACA CTCCACTTGC CCTTGTGAGA CACTTTGTCC CAGCACTTTA GGAATGCTGA	60
GGTCGGACCA GCCACATCTC ATGTGCAAGA TTGCCCAGCA GACATCAGGT CTGAGAGTTC	120
CCCTTTTAAA AAAGGGGACT TGCTTAAAAA AGAAGTCTAG CCACGATTGT GTAGAGCAGC	180
TGTGCTGTGC TGGAGATTCA CTTTGTGAGAG AGTTCTCCTC TGAGACCTGA TCTTTAGAGG	240
CTGGGCAGTC TTGCACATGA GATGGGGCTG GTCTGATCTC AGCACTCCTT AGTCTGCTTG	300
CCTCTCCAG GGCCCCAGCC TGGCCACACC TGCTTACAGG GCACTCTCAG ATGCCCATAC	360
CATAGTTTCT GTGCTAGTGG ACCGT	385

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ACTTAACCAG ATATATTTTT ACCCCAGATG GGGATATTCT TTGTAAAAAA TGAAAATAAA	60
GTTTTTTTAA TGG	73

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGGGCTC TCACCCTCCT CTCCTGCAGC	60
TCCAGCTTTG TGCTCTGCCT CTGAGGAGAC CATGGCCCAG CATCTGAGTA CCCTGCTGCT	120
CCTGCTGGCC ACCCTAGCTG TGGCCCTGGC CTGGAGCCCC AAGGAGGAGG ATAGGATAAT	180
CCCGGGTGGC ATCTATAACG CAGACCTCAA TGATGAGTGG GTACAGCGTG CCCTTCACTT	240
CGCCATCAGC GAGTATAACA AGGCCACCAA AGATGACTAC TACAGACGTC CGCTGCGGGT	300
ACTAAGAGCC AGGCAACAGA CCGTTGGGGG GGTGAATTAC TTCTTCGACG TAGAGGTGGG	360
CCGAACCATA TGTACCAAGT CCCAGCCCAA CTTGGACACC TGTGCCTTCC ATGAACAGCC	420
AGAACTGCAG AAGAAACAGT TGTGCTCTTT CGAGATCTAC GAAGTTCCTT GGGGAGAACA	480
GAANGTCCCT GGGTGAAATC CAGGTGTCAA GAAATCCTAN GGATCTGTTG CCAGGC	536

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGACCCCTA ACAGGGGCCC TCTCAGCCCT CTAATGACC TCCGGCCTAG CCATGTGATT	60
TCACTTCCAC TCCATAACGC TCCTCATACT AGGCCTACTA ACCAACACAC TAACCATATA	120
CCAATGATGG CGCGATGTAA CACGAGAAAG CACATACCAA GGCCACCACA CACCACCTGT	180
CCAAAAAGGC CTTTCGATACG GGATAATCCT ATTTATTACC TCAGAAGTTT TTTTCTTCGC	240
AGGGATTTT CTGAGCCTTT TACCACTCCA GCCTAGCCCC TACCCCCCAA CTAGGAGGGC	300
ACTGGCCCC AACAGGCATC ACCCCGCTAA ATCCCCTAGA AGTCCCCTC CTAAACACAT	360
CCGTATTACT CGCATCAGGA GTATCAATCA CTTGAGCTCA CCATAGTCTA ATAGAAAACA	420
ACCGAAACCA AATTATTCAA AGCACTGCTT ATTACAATT TACTGGGTCT CTATTTT	477

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AGAGCTATAG GTACAGTGTG ATCTCAGCTT TGCAAACACA TTTTCTACAT AGATAGTACT	60
AGGTATTAAT AGATATGTAA AGAAAGAAAT CACACCATTA ATAATGGTAA GATTGGTTTA	120
TGTGATTTTA GTGTATTTT TGGCACCCTT ATATATGTTT TCCAACTTT CAGCAGTGAT	180
ATTATTTCCA TAACTTAAAA AGTGAGTTTG AAAAAGAAAA TCTCCAGCAA GCATCTCATT	240
TAAATAAAGG TTTGTCTCTT TTAAAAATAC AGCAATATGT GACTTTTAA AAAAGCTGTC	300
AAATAGGTGT GACCCTACTA ATAATTATTA GAAATACATT TAAAAACATC GAGTACCTCA	360
AGTCAGTTTG CCTTGAAAAA TATCAATAT AACTCTTAGA GAAATGTACA TAAAAGAATG	420
CTTCGTAATT TTGGAGTANG AGGTTCCCTC CTCAATTTTG TATTTTAAA AAGTACATGG	480

TAAAAAAAAA AATTCACAAC AGTATATAAG GCTGTAAAAT GAAGAATTCT GCC

533

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 511 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TATTACGGAA AAACACACCA CATAATTCAA CTANCAAAGA ANACTGCTTC AGGGCGTGTA	60
AAATGAAAGG CTTCCAGGCA GTTATCTGAT TAAAGAACAC TAAAAGAGGG ACAAGGCTAA	120
AAGCCGCAGG ATGTCTACAC TATANCAGGC GCTATTTGGG TTGGCTGGAG GAGCTGTGGA	180
AAACATGGAN AGATTGGTGC TGGANATCGC CGTGGCTATT CCTCATGTGTT ATTACANAGT	240
GAGGTTCTCT GTGTGCCAC TGGTTTGAAA ACCGTTCTNC AATAATGATA GAATAGTACA	300
CACATGAGAA CTGAAATGGC CCAAACCCAG AAAGAAAGCC CAACTAGATC CTCAGAAAC	360
GCTTCTAGGG ACAATAACCG ATGAAGAAAA GATGGCCTCC TTGTGCCCC GTCTGTTATG	420
ATTTCTCTCC ATTGCAGCNA NAAACCCGTT CTTCTAAGCA AACNCAGGTG ATGATGGCNA	480
AAATACACCC CCTCTTGAAG NACCNGGAGG A	511

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 499 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CAGTGCCAGC ACTGGTGCCA GTACCAGTAC CAATAACAGT GCCAGTGCCA GTGCCAGCAC	60
CAGTGGTGGC TTCAGTGCTG GTGCCAGCCT GACCGCCACT CTCACATTTG GGCTCTTCGC	120
TGGCCTTGGT GGAGCTGGTG CCAGCACCAG TGGCAGCTCT GGTGCCTGTG GTTTCTCCTA	180
CAAGTGAGAT TTAGATATT GTTAATCCTG CCAGTCTTTC TCTTCAAGCC AGGGTGCATC	240
CTCAGAAACC TACTCAACAC AGCACTCTAG GCAGCCACTA TCAATCAATT GAAGTTGACA	300
CTCTGCATTA AATCTATTTG CCATTCTGA AAAAAAAAAA AAAAAAAGGG CGGCCGCTCG	360
ANTCTAGAGG GCCCGTTTAA ACCCGCTGAT CAGCCTCGAC TGTGCCTTCT ANTGGCCAGC	420
CATCTGTTGT TTGCCCTCC CCCGNTGCCT TCCTTGACCC TGGAAAGTGC CACTCCCACT	480
GTCTTTTCTT AANTAAAAT	499

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 537 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TTTCATAGGA	GAACACACTG	AGGAGATACT	TGAAGAATTT	GGATTCAGCC	GCGAAGAGAT	60
TTATCAGCTT	AACTCAGATA	AAATCATTGA	AAGTAATAAG	GTAAGGCTA	GTCTCTAAT	120
TCCAGGCCCA	CGGCTCAAGT	GAATTTGAAT	ACTGCATTTA	CAGTGTAGAG	TAACACATAA	180
CATTGTATGC	ATGGAAACAT	GGAGGAACAG	TATTACAGTG	TCCTACCACT	CTAATCAAGA	240
AAAGAATTAC	AGACTCTGAT	TCTACAGTGA	TGATTGAATT	CTAAAAATGG	TAATCATTAG	300
GGCTTTTGAT	TTATAANACT	TTGGGTACTT	ATACTAAATT	ATGGTAGTTA	TACTGCCTTC	360
CAGTTTGCTT	GATATATTG	TTGATATTAA	GATTCTTGAC	TTATATTTTG	AATGGGTTCT	420
ACTGAAAAAN	GAATGATATA	TTCTTGAAGA	CATCGATATA	CATTTATTTA	CACCTTTGAT	480
TCTACAATGT	AGAAAATGAA	GGAAATGCCC	CAAATTGTAT	GGTGATAAAA	GTCCCGT	537

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CAAANACAAT	TGTTCAAAAG	ATGCAAATGA	TACACTACTG	CTGCAGCTCA	CAAACACCTC	60
TGCATATTAC	ACGTACCTCC	TCCTGCTCCT	CAAGTAGTGT	GGTCTATTTT	GCCATCATCA	120
CCTGCTGTCT	GCTTAGAAGA	ACGGCTTTCT	GCTGCAANGG	AGAGAAATCA	TAACAGACGG	180
TGGCACAAGG	AGGCCATCTT	TTCCCTCATCG	GTTATTGTCC	CTAGAAGCGT	CTTCTGAGGA	240
TCTAGTTGGG	CTTCTTTTCT	GGGTTTGGGC	CATTTCANTT	CTCATGTGTG	TACTATTCTA	300
TCATTATTGT	ATAACGGTTT	TCAAACNGT	GGGCACNCAG	AGAACCTCAC	TCTGTAATAA	360
CAATGAGGAA	TAGCCACGGT	GATCTCCAGC	ACCAAATCTC	TCCATGTTNT	TCCAGAGCTC	420
CTCCAGCCAA	CCCAAATAGC	CGCTGCTATN	GTGTAGAACA	TCCCTGN		467

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

AAGCTGACAG	CATTGCGGCC	GAGATGTCTC	GCTCCGTGGC	CTTAGCTGTG	CTCGCGCTAC	60
TCTCTCTTTT	TGGCCTGGAG	GCTATCCAGC	GTAATCCAAA	GATTGAGGTT	TACTCACGTC	120
ATCCAGCAGA	GAATGGAAAG	TCAAATTTCC	TGAATTGCTA	TGTGTCTGGG	TTTCATCCAT	180
CCGACATTGA	AGTTGACTTA	CTGAAGAATG	GAGAGAGAAT	TGAAAAAGTG	GAGCATTGAG	240
ACTTGTCTTT	CAGCAAGGAC	TGGTCTTTCT	ATCTCTTGTA	CTACACTGAA	TTCAACCCCA	300
CTGAAAAAGA	TGAGTATGCC	TGCCGTGTGA	ACCATGTGAC	TTTGTCACAG	CCCAAGATNG	360

TTNAGTGGGA TCGANACATG TAAGCAGCAN CATGGGAGGT

400

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTGGAGTGCC TTGGTGTTC AAGCCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT	60
CCAGCTGCCC CGGCGGGGGA TGCGAGGCTC GGAGCACCCT TGCCCGGCTG TGATTGCTGC	120
CAGGCACTGT TCATCTCAGC TTTTCTGTCC CTTTGCTCCC GGCAAGCGCT TCTGCTGAAA	180
GTTCATATCT GGAGCCTGAT GTCTTAACGA ATAAAGGTCC CATGCTCCAC CCGAAAAAAA	240
AAAAAAAA	248

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCCAA CACAATGGCT ACCTTTAACA	60
TCACCCAGAC CCCGCCCTGC CCGTGCCCCA CGCTGCTGCT AACGACAGTA TGATGCTTAC	120
TCTGCTACTC GGAAACTATT TTTATGTAAT TAATGTATGC TTTCTTGTTT ATAAATGCCT	180
GATTTAAAAA AAAAAAAAAA A	201

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 552 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TCCTTTTGTG AGGTTTTTGA GACAACCCTA GACCTAAACT GTGTCACAGA CTTCTGAATG	60
TTTAGGCAGT GCTAGTAATT TCCTCGTAAT GATTCTGTTA TTACTTTCCT ATTCTTTATT	120
CCTCTTTCTT CTGAAGATTA ATGAAGTTGA AAATTGAGGT GGATAAATAC AAAAAGGTAG	180

TGTGATAGTA TAAGTATCTA AGTGCAGATG AAAGTGTGTT ATATATATCC ATTCAAAATT	240
ATGCAAGTTA GTAATTACTC AGGGTTAACT AAATTACTTT AATATGCTGT TGAACCTACT	300
CTGTTCTTGG GCTAGAAAAA ATTATAAACA GGACTTTGTT AGTTTGGGAA GCCAAATTGA	360
TAATATTCTA TGTTCTAAAA GTTGGGCTAT ACATAAANTA TNAAGAAATA TGGAAATTTTA	420
TTCACAGGAA TATGGGGTTC ATTTATGAAT ANTACCCGGG ANAGAAGTTT TGANTNAAAC	480
CNGTTTTGGT TAATACGTTA ATATGTCCTN AATNAACAAG GCNTGACTTA TTTCCAAAAA	540
AAAAAAAAAA AA	552

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ACAGGGATTG GAGATGCTAA GGCCCCAGAG ATCGTTTGAT CCAACCCTCT TATTTTCAGA	60
GGGGAAAAATG GGGCCTAGAA GTTACAGAGC ATCTAGCTGG TGCGCTGGCA CCCCTGGCCT	120
CACACAGACT CCCGAGTAGC TGGGACTACA GGCACACAGT CACTGAAGCA GGCCCTGTTT	180
GCAATTCACG TTGCCACCTC CAACTTAAAC ATTCTTCATA TGTGATGTCC TTAGTCACTA	240
AGGTTAAACT TTCCACCCCA GAAAAGGCAA CTTAGATAAA ATCTTAGAGT ACTTTCATAC	300
TCTTCTAAGT CCTCTTCCAG CCTCACTTTG AGTCCTCCTT GGGGGTTGAT AGGAANTNTC	360
TCTTGGCTTT TCAATAAAA TCTCTATCCA TCTCATGTTT AATTTGGTAC GCNTAAAAAT	420
GCTGAAAAAA TTAAATGTT CTGGTTTCNC TTTAAAAAAA AAAAAAAAAA AAAAAA	476

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTTTTTTTTG TATGCCNTCN CTGTGGNGTT ATTGTTGCTG CCACCCTGGA GGAGCCCAGT	60
TTCTTCTGTA TCTTTCTTTT CTGGGGGATC TTCCTGGCTC TGCCCCCTCA TTCCCAGCCT	120
CTCATCCCCA TCTTGCACTT TTGCTAGGGT TGGAGGCGCT TTCCTGGTAG CCCCTCAGAG	180
ACTCAGTCAG CGGGAATAAG TCCTAGGGGT GGGGGGTGTG GCAAGCCGGC CT	232

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AGGCGGGAGC AGAAGCTAAA GCCAAAGCCC AAGAAGAGTG GCAGTGCCAG CACTGGTGCC	60
AGTACCAGTA CCAATAACAT GCCAGTGCCA GTGCCAGCAC CAGTGGTGGC TTCAGTGCTG	120
GTGCCAGCCT GACCGCCACT CTCACATTG GGCTCTTCGC TGGCCTTGGT GGAGCTGGTG	180
CCAGCACCAG TGGCAGCTCT GGTGCCTGTG GTTTCTCCTA CAAGTGAGAT TTAGATATT	240
GTTAATCCTG CCAGTCTTTC TCTTCAAGCC AGGGTGCATC CTCAGAAACC TACTCAACAC	300
AGCACTCTNG GCAGCCACTA TCAATCAATT GAAGTTGACA CTCTGCATTA AATCTATTTG	360
CCATTTCAAA AAAAAAAAAA AAA	383

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTCCTC CAGTATTACC TCAACGAGCA	60
GGGAGATCGA GTCTATACGC TGAAGAAATT TGACCCGATG GGACAACAGA CCTGCTCAGC	120
CCATCCTGCT CGGTTCTCCC CAGATGACAA ATACTCTCGA CACCGAATCA CCATCAAGAA	180
ACGCTTCAAG GTGCTCATGA CCCAGCAACC GCGCCCTGTC CTCTGAGGGT CCTTAAACTG	240
ATGTCTTTTC TGCCACCTGT TACCCCTCGG AGACTCCGTA ACCAAACTCT TCGGACTGTG	300
AGCCCTGATG CCTTTTGTGCC AGCCATACTC TTTGGCNTCC AGTCTCTCGT GGCGATTGAT	360
TATGCTGTG TGAGGCAATC ATGGTGGCAT CACCCATNAA GGAACACAT TTGANTTTT	420
TTTCNCATAT TTAAATTAC NACCAGAATA NTTCAGAATA AATGAATTGA AAAACTCTTA	480
AAAAAAAAA AAAA	494

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GCTGGTAGCC TATGGCGTGG CCACGGANGG GCTCCTGAGG CACGGGACAG TGACTTCCCA	60
AGTATCCTGC GCCGCGTCTT CTACCGTCCC TACCTGCAGA TCTTCGGGCA GATTCCCCAG	120
GAGGACATGG ACGTGGCCCT CATGGAGCAC AGCAACTGCT CGTCGGAGCC CGGCTTCTGG	180
GCACACCTC CTGGGGCCCA GCGGGGCACC TGCGTCTCCC AGTATGCCAA CTGGCTGGTG	240
GTGCTGCTCC TCGTCATCTT CCTGCTCGTG GCCAACATCC TGCTGGTCAC TTGCTCATTG	300
CCATGTTTCA TACACATTG GCCAAAGTAC AGGGCAACAG CNATCTCTAC TGGGAAGGCC	360
AGCGTTNCCG CCTCATCCGG	380

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 481 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

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GAGTTAGCTC CTCCACAACC TTGATGAGGT CGTCTGCAGT GGCCTCTCGC TTCATACCGC      60
TNCCATCGTC ATACTGTAGG TTTGCCACCA CCTCCTGCAT CTTGGGGCGG CTAATATCCA      120
GGAAACTCTC AATCAAGTCA CCGTCNATNA AACCTGTGGC TGGTTCTGTC TTCCGCTCGG      180
TGTGAAAGGA TCTCCAGAAG GAGTGCTCGA TCTTCCCCAC ACTTTTGATG ACTTTATTGA      240
GTCGATTCTG CATGTCCAGC AGGAGGTTGT ACCAGCTCTC TGACAGTGAG GTCACCAGCC      300
CTATCATGCC NTTGAACGTG CCGAAGAACA CCGAGCCTTG TGTGGGGGGT GNAGTCTCAC      360
CCAGATTCTG CATTACCAGA NAGCCGTGGC AAAAGANATT GACAACTCGC CCAGGNNGAA      420
AAAGAACACC TCCTGGAAGT GCTNGCCGCT CCTCGTCCNT TGGTGGNNGC GCNTNCCTTT      480
T

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(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 472 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

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AACATCTTCC TGTATAATGC TGTGTAATAT CGATCCGATN TTGTCTGCTG AGAATTCATT      60
ACTTGGAATA GCAACTTNA GCCTGGACAC TGGTATTAAA ATTCACAATA TGCAACACTT      120
TAAACAGTGT GTCAATCTGC TCCCTTACTT TGTATCACC AGTCTGGGAA TAAGGGTATG      180
CCCTATTAC ACCTGTTAAA AGGGCGCTAA GCATTTTTGA TTCAACATCT TTTTTTTTGA      240
CACAAGTCCG AAAAAAGCAA AAGTAAACAG TTNTTAATTT GTTAGCCAAT TCACTTTCTT      300
CATGGGACAG AGCCATTTGA TTTAAAAAGC AAATTGCATA ATATTGAGCT TTGGGAGCTG      360
ATATNTGAGC GGAAGANTAG CCTTTCTACT TCACCAGACA CAACTCCTTT CATATTGGGA      420
TGTTNACNAA AGTTATGTCT CTTACAGATG GGATGCTTTT GTGGCAATTC TG          472

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(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 413 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

AGAAACCACT	ATCTCTNAAA	ACAACCTCTC	ATACCTTGTG	GACCTAATTT	TGTGTGCGTG	60
TGTGTGTGCG	CGCATATTAT	ATAGACAGGC	ACATCTTTTT	TACTTTTGTA	AAAGCTTATG	120
CCTCTTTGGT	ATCTATATCT	GTGAAAGTTT	TAATGATCTG	CCATAATGTC	TTGGGGACCT	180
TTGTCTTCTG	TGTAAATGGT	ACTAGAGAAA	ACACCTATNT	TATGAGTCAA	TCTAGTTNGT	240
TTTATTCGAC	ATGAAGGAAA	TTTCCAGATN	ACAACACTNA	CAAACCTCTC	CTTGACTAGG	300
GGGGACAAAG	AAAAGCANAA	CTGAACATNA	GAAACAATTN	CCTGGTGAGA	AATTNCATAA	360
ACAGAAATTG	GGTNGTATAT	TGAAANANNG	CATCATTNAA	ACGTTTTTTT	TTT	413

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CGCAGCGGGT	CCTCTCTATC	TAGCTCCAGC	CTCTCGCCTG	CCCCACTCCC	CGCGTCCCGC	60
GTCCTAGCCN	ACCATGGCCG	GGCCCCGTG	CGCCCCGCTG	CTCCTGCTGG	CCATCCTGGC	120
CGTGGCCCTG	GCGGTGAGCC	CCGCGGCCGG	CTCCAGTCCC	GGCAAGCCGC	CGCGCCTGGT	180
GGGAGGCCCA	TGGACCCCGC	GTGAAGAAG	AAGGTGTGCG	GCGTGCACTG	GACTTTGCCG	240
TCGGCNANTA	CAACAAACCC	GCAACNACTT	TTACCNAGCN	CGCGCTGCAG	GTTGTGCCGC	300
CCCAANCAAA	TTGTTACTNG	GGGTAANTAA	TTCTTGGAAG	TTGAACCTGG	GCCAAACNNG	360
TTTACCAGAA	CCNAGCCAAT	TNGAACAAAT	NCCCTCCAT	AACAGCCCCT	TTTAAAAAGG	420
GAANCANTCC	TGNTCTTTTC	CAAATTTT				448

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GAATTTTGTG	CACTGGCCAC	TGTGATGGAA	CCATTGGGCC	AGGATGCTTT	GAGTTTATCA	60
GTAGTGATTC	TGCCAAAGTT	GGTGTGTGAA	CATGAGTATG	TAAAATGTCA	AAAAATTAGC	120
AGAGGTCTAG	GTCTGCATAT	CAGCAGACAG	TTTGTCCGTG	TATTTTGTAG	CCTTGAAGTT	180
CTCAGTGACA	AGTTNNTTCT	GATGCGAAGT	TCTNATTCCA	GTGTTTTAGT	CCTTTGCATC	240
TTTATGTGTT	AGACTTGCCT	CTNTNAAATT	GCTTTTGTNT	TCTGCAGGTA	CTATCTGTGG	300
TTTAACAAAA	TAGAANNACT	TCTCTGCTTN	GAANATTGTA	ATATCTTACA	TCTNAAAATN	360
AATTCTCTCC	CCATANNAAA	ACCCANGCCC	TTGGGANAAT	TTGAAAAANG	GNTCCTTCNN	420
AATTCNNANA	ANTTCAGNTN	TCATACAACA	NAACNGGANC	CCC		463

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

AGGGATTGAA GGTCTNTTNT ACTGTCGGAC TGTTCANCCA CCAACTCTAC AAGTTGCTGT	60
CTTCCACTCA CTGTCTGTAA GCNTNTTAAAC CCAGACTGTA TCTTCATAAA TAGAACAAAT	120
TCTTCACCAG TCACATCTTC TAGGACCTTT TTGGATTGAG TTAGTATAAG CTCTTCCACT	180
TCCTTTGTTA AGACTTCATC TGGTAAAGTC TTAAGTTTTG TAGAAAGGAA TTTAATTGCT	240
CGTTCTCTAA CAATGTCCTC TCCTTGAAGT ATTTGGCTGA ACAACCCACC TNAAGTCCCT	300
TTGTGCATCC ATTTTAAATA TACTTAATAG GGCATTGGTN CACTAGGTTA AATTCTGCAA	360
GAGTCATCTG TCTGCAAAAG TTGCGTTAGT ATATCTGCCA	400

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 480 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAGCTCGGAT CCAATAATCT TTGTCTGAGG GCAGCACACA TATNCAGTGC CATGGNAACT	60
GGTCTACCCC ACATGGGAGC AGCATGCCGT AGNTATATAA GGTCATTCCC TGAGTCAGAC	120
ATGCCTCTTT GACTACCGTG TGCCAGTGCT GGTGATTCTC ACACACCTCC NNCCGCTCTT	180
TGTGGAAAAA CTGGCACTTG NCTGGAAC TA GCAAGACATC ACTTACAAAT TCACCCACGA	240
GACACTTGAA AGGTGTAACA AAGCGACTCT TGCATTGCTT TTTGTCCCTC CGGCACCACT	300
TGTCAATACT AACCCGCTGG TTTGCCTCCA TCACATTTGT GATCTGTAGC TCTGGATACA	360
TCTCCTGACA GTACTGAAGA ACTTCTTCTT TTGTTTCAAA AGCAACTCTT GGTGCCTGTT	420
NGATCAGGTT CCCATTTCCC AGTCCGAATG TTCACATGGC ATATNTTACT TCCCACAAAA	480

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATACAGCCCA	NATCCCACCA	CGAAGATGCG	CTTGTTGACT	GAGAACCTGA	TGCGGTCACT	60
GGTCCCGCTG	TAGCCCCAGC	GACTCTCCAC	CTGCTGGAAG	CGGTTGATGC	TGCACTCCTT	120
CCCACGCAGG	CAGCAGCGGG	GCCGGTCAAT	GAAGTCCACT	CGTGGCTTGG	GTTTGACGGT	180
TAANTGCAGG	AAGAGGCTGA	CCACCTCGCG	GTCCACCAGG	ATGCCCCGACT	GTGCGGGACC	240
TGCAGCGAAA	CTCCTCGATG	GTCATGAGCG	GGAAGCGAAT	GANGCCCAGG	GCCTTGCCCA	300
GAACCTTCCG	CCTGTTCTCT	GGCGTCACCT	GCAGCTGCTG	CCGCTNACAC	TGGCCTCGG	360
ACCAGCGGAC	AAACGGCGTT	GAACAGCCGC	ACCTCACGGA	TGCCCANTGT	GTCGCGCTCC	420
AGGAACGGCN	CCAGCGTGTC	CAGGTCAATG	TCGGTGAANC	CTCCGCGGGT	AATGGCG	477

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAACGGCTGG	ACCTTGCTC	GCATTGTGCT	GCTGGCAGGA	ATACCTTGGC	AAGCAGCTCC	60
AGTCCGAGCA	GCCCCAGACC	GCTGCCGCC	GAAGCTAAGC	CTGCCTCTGG	CCTTCCCCTC	120
CGCCTCAATG	CAGAACCAANT	AGTGGGAGCA	CTGTGTTTAG	AGTTAAGAGT	GAACACTGTN	180
TGATTTTACT	TGGGAATTTT	CTCTGTTATA	TAGCTTTTCC	CAATGCTAAT	TTCCAAACAA	240
CAACAACAAA	ATAACATGTT	TGCCTGTINA	GTTGTATAAA	AGTANGTGAT	TCTGTATNTA	300
AAGAAAATAT	TACTGTTACA	TATACTGCTT	GCAANTTCTG	TATTTATTGG	TNCTCTGGAA	360
ATAAATATAT	TATTAAA					377

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCCTTTGAGG	GGTTAGGGTC	CAGTTCACAG	TGGAAGAAAC	AGGCCAGGAG	AANTGCGTGC	60
CGAGCTGANG	CAGATTTCCC	ACAGTGACCC	CAGAGCCCTG	GGCTATAGTC	TCTGACCCCT	120
CCAAGGAAAG	ACCACCTTCT	GGGGACATGG	GCTGGAGGGC	AGGACCTAGA	GGCACCAGG	180
GAAGGCCCA	TTCCGGGGCT	GTTCCCCGAG	GAGGAAGGGA	AGGGGCTCTG	TGTGCCCCCC	240
ACGAGGAANA	GGCCCTGANT	CCTGGGATCA	NACACCCCTT	CACGTGTATC	CCCACACAAA	300
TGCAAGCTCA	CCAAGGTCCC	CTCTCAGTCC	CTTCCCTACA	CCCTGAACGG	NCACTGGCCC	360
ACACCCACCC	AGANCANCCA	CCCGCCATGG	GGAATGTNCT	CAAGGAATCG	CNGGGCAACG	420
TGGACTCTNG	TCCCNNAAGG	GGGCAGAATC	TCCAATAGAN	GGANNGAACC	CTTGCTNANA	480
AAAAAAAANA	AAAAA					495

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GGTACTTGG	TTTCATTGCC	ACCACTTAGT	GGATGTCATT	TAGAACCATT	TTGTCTGCTC	60
CCTCTGGAAG	CCTTGCGCAG	AGCGGACTTT	GTAATTGTTG	GAGAATAACT	GCTGAATTTT	120
TAGCTGTTTT	GAGTTGATTC	GCACCACTGC	ACCACAACCTC	AATATGAAAA	CTATTTNACT	180
TATTTATTAT	CTTGTGAAAA	GTATACAATG	AAAATTTTGT	TCATACTGTA	TTTATCAAGT	240
ATGATGAAAA	GCAATAGATA	TATATTCTTT	TATTATGTTN	AATTATGATT	GCCATTATTA	300
ATCGGCAAAA	TGTGGAGTGT	ATGTTCTTTT	CACAGTAATA	TATGCCTTTT	GTAACCTCAC	360
TTGGTTATTT	TATTGTAAAT	GAATTACAAA	ATTCTTAATT	TAAGAAAATG	GTANGTTATA	420
TTTANTTCAN	TAATTTCTTT	CCTTGTTTAC	GTTAATTTTG	AAAAGAATGC	AT	472

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTGAAGCATT	TCTTCAAAC	TNTCTACTTT	TGTCATTGAT	ACCTGTAGTA	AGTTGACAAT	60
GTGGTGAAAT	TTCAAAATTA	TATGTAACTT	CTACTAGTTT	TACTTTCTCC	CCCAAGTCTT	120
TTTTAACTCA	TGATTTTAC	ACACACAATC	CAGAACTTAT	TATATAGCCT	CTAAGTCTTT	180
ATTCTTCACA	GTAGATGATG	AAAGAGTCCT	CCAGTGTCTT	GNGCANAATG	TTCTAGNTAT	240
AGCTGGATAC	ATACNGTGGG	AGTTCTATAA	ACTCATACCT	CAGTGGGACT	NAACCAAAAT	300
TGTGTTAGTC	TCAATTCCTA	CCACACTGAG	GGAGCCTCCC	AAATCACTAT	ATTCTTATCT	360
GCAGGTACTC	CTCCAGAAAA	ACNGACAGGG	CAGGCTTGCA	TGAAAAAGTN	ACATCTGCGT	420
TACAAAGTCT	ATCTTCCTCA	NANGTCTGTN	AAGGAACAAT	TTAATCTTCT	AGCTTT	476

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ACTCTTTCTA	ATGCTGATAT	GATCTTGAGT	ATAAGAATGC	ATATGTCACT	AGAATGGATA	60
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AAATAATGCT	GCAAACCTTAA	TGTTCTTATG	CAAAATGGAA	CGCTAATGAA	ACACAGCTTA	120
CAATCGCAAA	TCAAAACTCA	CAAGTGCTCA	TCTGTTGTAG	ATTTAGTGTA	ATAAGACTTA	180
GATTGTGCTC	CTTCGGATAT	GATTGTTTCT	CANATCTTGG	GCAATNTTCC	TTAGTCAAAT	240
CAGGCTACTA	GAATTCTGTT	ATTGGATATN	TGAGAGCATG	AAATTTTTAA	NAATACACTT	300
GTGATTATNA	AATTAATCAC	AAATTTCACT	TATACCTGCT	ATCAGCAGCT	AGAAAAACAT	360
NTNNTTTTTA	NATCAAAGTA	TTTTGTGTTT	GGAANTGTNN	AAATGAAATC	TGAATGTGGG	420
TTCNATCTTA	TTTTTTCN	GACNACTANT	TNCTTTTTTA	GGGNCTATTC	TGANCCATC	479

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AGTGACTTGT	CCTCCAACAA	AACCCCTTGA	TCAAGTTTGT	GGCACTGACA	ATCAGACCTA	60
TGCTAGTTCC	TGTCATCTAT	TCGCTACTAA	ATGCAGACTG	GAGGGGACCA	AAAAGGGGCA	120
TCAACTCCAG	CTGGATTATT	TTGGAGCCTG	CAAATCTATT	CCTACTTGTA	CGGACTTTGA	180
AGTGATTCAG	TTTCCTCTAC	GGATGAGAGA	CTGGCTCAAG	AATATCCTCA	TGCAGCTTTA	240
TGAAGCCACT	CTGAACACGC	TGGTTATCTA	GATGAGAACA	GAGAAATAAA	GTCAGAAAAT	300
TTACCTGGAG	AAAAGAGGCT	TTGGCTGGGG	ACCATCCCAT	TGAACCTTCT	CTTAAGGACT	360
TTAAGAAAAA	CTACCACATG	TTGTGTATCC	TGGTGCCGGC	CGTTTATGAA	CTGACCACCC	420
TTTGGAATAA	TCTTGACGCT	CCTGAACTTG	CTCCTCTGCG	A		461

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTGGCCGCGC	GCAGGTGTTT	CCTCGTACCG	CAGGGCCCCC	TCCCTTCCCC	AGGCGTCCCT	60
CGGCGCCTCT	GCGGGCCCGA	GGAGGAGCGG	CTGGCGGGTG	GGGGGAGTGT	GACCCACCCT	120
CGGTGAGAAA	AGCCTTCTCT	AGCGATCTGA	GAGGCGTGCC	TTGGGGGTAC	C	171

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CGGCCGCAAG TGCAACTCCA GCTGGGGCCG TGCGGACGAA GATTCTGCCA GCAGTTGGTC	60
CGACTGCGAC GACGGCGGCG GCGACAGTCG CAGGTGCAGC GCGGGCGCCT GGGGTCTTGC	120
AAGGCTGAGC TGACGCCGCA GAGGTCGTGT CACGTCCCAC GACCTTGACG CCGTCGGGGA	180
CAGCCGGAAC AGAGCCCGGT GAAGCGGGAG GCCTCGGGGA GCCCTCGGG AAGGGCGGGC	240
CGAGAGATAC GCAGGTGCAG GTGGCCGCC	269

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TTTTTTTTTT TTTTGGAATC TACTGCGAGC ACAGCAGGTC AGCAACAAGT TTATTTTGCA	60
GCTAGCAAGG TAACAGGGTA GGGCATGGTT ACATGTTTCC GTCAACTTCC TTTGTCTGGG	120
TTGATTGGTT TGTCTTTATG GGGGCGGGT GGGGTAGGG AAACGAAGCA AATAACATGG	180
AGTGGGTGCA CCCTCCCTGT AGAACCTGGT TACAAAGCTT GGGGCAGTTC ACCTGGTCTG	240
TGACCGTCAT TTTCTTGACA TCAATGTTAT TAGAAGTCAG GATATCTTTT AGAGAGTCCA	300
CTGTTCTGGA GGGAGATTAG GGTTCCTTGC CAAATCCAAC AAAATCCACT GAAAAAGTTG	360
GATGATCAGT ACGAATACCG AGGCATATTC TCATATCGGT GGCCA	405

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT	60
GGCACTTAAT CCATTTTAT TTCAAAATGT CTACAAATTT AATCCCATTA TACGGTATTT	120
TCAAAATCTA AATTATTCAA ATTAGCCAAA TCCTTACCAA ATAATACCCA AAAATCAAAA	180
ATATACTTCT TTCAGCAAAC TTGTTACATA AATTAAAAAA ATATATACGG CTGGTGTTTT	240
CAAAGTACAA TTATCTTAAC ACTGCAACA TTTTAAGGAA CTAAATATAA AAAAAACACT	300
CCGCAAAGGT TAAAGGGAAC AACAAATTCT TTTACAACAC CATTATAAAA ATCATATCTC	360
AAATCTTAGG GGAATATATA CTTACACG GATCTTAAT TTTACTCACT TTGTTTATTT	420
TTTAAACCA TTGTTTGGGC CCAACACAAT GGAATCCCC CTGGACTAGT	470

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TTTTTTTTTT TTTTTTTTGA CCCCCCTCTT ATAAAAAACA AGTTACCATT TTATTTTACT	60
TACACATATT TATTTTATAA TTGGTATTAG ATATTCAAAA GGCAGCTTTT AAAATCAAAC	120
TAAATGGAAA CTGCCTTAGA TACATAATTC TTAGGAATTA GCTTAAAATC TGCCTAAAGT	180
GAAAATCTTC TCTAGCTCTT TTGACTGTAA ATTTTGTACT CTTGTAAAAC ATCCAAATTC	240
ATTTTCTTGG TCTTTAAAAT TATCTAATCT TTCCATTTTT TCCCTATTCC AAGTCAATTT	300
GCTTCTCTAG CCTCATTTCC TAGCTCTTAT CTACTATTAG TAAGTGGCTT TTTTCCTAAA	360
AGGGAAGAAA GGAAGAGAAA TGGCACACAA AACAAACATT TTATATTCAT ATTTCTACCT	420
ACGTTAATAA AATAGCATT TGTGAAGCCA GCTCAAAAGA AGGCTTAGAT CCTTTTATGT	480
CCATTTTAGT CACTAAACGA TATCAAAGTG CCAGAATGCA AAAGGTTTGT GAACATTTAT	540
TCAAAAGCTA ATATAAGATA TTTCACATAC TCATCTTTCT G	581

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TTTTTTTTTTT TTTTTTTTTT TTTTCTCTT CTTTTTTTTT GAAATGAGGA TCGAGTTTTT	60
CACTCTCTAG ATAGGGCATG AAGAAAACCTC ATCTTTCCAG CTTTAAAATA ACAATCAAAT	120
CTCTTATGCT ATATCATATT TTAAGTTAAA CTAATGAGTC ACTGGCTTAT CTTCTCCTGA	180
AGGAAATCTG TTCATTCTTC TCATTCATAT AGTTATATCA AGTACTACCT TGCATATTGA	240
GAGGTTTTTC TTCTCTATTT ACACATATAT TTCCATGTGA ATTTGTATCA AACCTTTTAT	300
TTTCATGCAA CTAGAAAATA ATGTTTCTTT TGCATAAGAG AAGAGAACAA TATAGCATT	360
CAAACTGCT CAAATTGTTT GTTAAGTTAT CCATTATAAT TAGTTGGCAG GAGCTAATAC	420
AAATCACATT TACGACAGCA ATAATAAAC TGAAGTACCA GTTAAATATC CAAAATAATT	480
AAAGGAACAT TTTTAGCCTG GGTATAATTA GCTAATTCAC TTTACAAGCA TTTATTAGAA	540
TGAATTCACA TGTTATTATT CCTAGCCCAA CACAATGG	578

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TTTTTTTTTT	TTTTTCAGTA	ATAATCAGAA	CAATATTTAT	TTTTATATTT	AAAATTCATA	60
GAAAAGTGCC	TTACATTTAA	TAAAAGTTTG	TTTCTCAAAG	TGATCAGAGG	AATTAGATAT	120
GTCTTGAACA	CCAATATTAA	TTTGAGGAAA	ATACACCAA	ATACATTAA	TAAATTATTT	180
AAGATCATAG	AGCTTGTAAG	TGAAAAGATA	AAATTTGACC	TCAGAAACTC	TGAGCATTAA	240
AAATCCACTA	TTAGCAAATA	AATTACTATG	GACTTCTTGC	TTTAATTTTG	TGATGAATAT	300
GGGGTGTCAC	TGGTAAACCA	ACACATTCTG	AAGGATACAT	TACTTAGTGA	TAGATTCTTA	360
TGTACTTTGC	TAATACGTGG	ATATGAGTTG	ACAAGTTTCT	CTTTCTTCAA	TCTTTTAAGG	420
GGCGAGAAAT	GAGGAAGAAA	AGAAAAGGAT	TACGCATACT	GTTCTTTCTA	TGGAAGGATT	480
AGATATGTTT	CCTTTGCCAA	TATTAAAAAA	ATAATAATGT	TTACTACTAG	TGAAACCC	538

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TTTTTTTTTT	TTTTTTAGTC	AAGTTTCTAT	TTTTATTATA	ATTAAAGTCT	TGGTCATTTT	60
ATTTATTAGC	TCTGCAACTT	ACATATTTAA	ATTAAAGAAA	CGTTTTAGAC	AACTGTACAA	120
TTTATAAATG	TAAGGTGCCA	TTATTGAGTA	ATATATTCCT	CCAAGAGTGG	ATGTGTCCCT	180
TCTCCCACCA	ACTAATGAAC	AGCAACATTA	GTTTAATTTT	ATTAGTAGAT	ATACACTGCT	240
GCAAACGCTA	ATTCTCTTCT	CCATCCCCAT	GTGATATTGT	GTATATGTGT	GAGTTGGTAG	300
AATGCATCAC	AATCTACAAT	CAACAGCAAG	ATGAAGCTAG	GCTGGGCTTT	CGGTGAAAT	360
AGACTGTGTC	TGTCTGAATC	AAATGATCTG	ACCTATCCTC	GGTGGCAAGA	ACTCTTCGAA	420
CCGCTTCCTC	AAAGGCGCTG	CCACATTTGT	GGCTCTTTGC	ACTTGTTTCA	AAA	473

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CGCCATGGCA	CTGCAGGCA	TCTCGGTCAT	GGAGCTGTCC	GGCCTGGCCC	CGGGCCCGTT	60
CTGTGCTATG	GTCCTGGCTG	ACTTCGGGGC	GCGTGTGCTA	CGCGTGGACC	GGCCCGGCTC	120
CCGCTACGAC	GTGAGCCGCT	TGGGCCGGGG	CAAGCGCTCG	CTAGTGTGCTG	ACCTGAAGCA	180
GCCGCGGGGA	GCCGCCGTGC	TGCGGCGTCT	GTGCAAGCGG	TGGATGTGTC	TGCTGGAGCC	240
CTTCCGCCGC	GGTGTATGCG	AGAACTCCA	GCTGGGCCCA	GAGATTCTGC	AGCGGGAAAA	300
TCCAAGGCTT	ATTTATGCCA	GGCTGAGTGG	ATTTGGCCAG	TCAGGAAGCT	TCTGCCGGTT	360
AGCTGGCCAC	GATATCAACT	ATTTGGCTTT	GTCAGGTGTT	CTCTCAAAAA	TTGGCAGAAG	420
TGGTGAGAAT	CCGTATGCCC	CGCTGAATCT	CCTGGCTGAC	TTTGCTGGTG	GTGGCCTTAT	480
GTGTGCACTG	GGCATTATAA	TGGCTCTTTT	TGACCGACA	CGCACTGACA	AGGGTCAGGT	540

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CATTGATGCA AATATGGTGG AAGGAACAGC ATATTTAAGT TCTTTTCTGT GGAAAACTCA      600
GAAATCGAGT CTGTGGGAAG CACCTCGAGG ACAGAACATG TTGGATGGTG GAGCACCTTT      660
CTATACGACT TACAGGACAG CAGATGGGGA ATTCATGGCT GTTGGAGCAA TAGAACCCCA      720
GTTCTACGAG CTGCTGATCA AAGGACTTGG ACTAAAGTCT GATGAACTTC CCAATCAGAT      780
GAGCATGGAT GATTGGCCAG AAATGAAGAA GAAGTTTGCA GATGTATTTG CAAAGAAGAC      840
GAAGGCAGAG TGGTGTCAAA TCTTTGACGG CACAGATGCC TGTGTGACTC CGGTTCTGAC      900
TTTTGAGGAG GTTGTTTCATC ATGATCACAA CAAGGAACGG GGCTCGTTTA TCACCAGTGA      960
GGAGCAGGAC GTGAGCCCCC GCCCTGCACC TCTGCTGTTA AACACCCCAG CCATCCCTTC     1020
TTTCAAAAGG GATCCTTTCA TAGGAGAACA CACTGAGGAG ATACTTGAAG AATTGGAATT     1080
CAGCCGCGAA GAGATTTATC AGCTTAACTC AGATAAAATC ATTGAAAGTA ATAAGGTAAA     1140
AGCTAGTCTC TAACTTCCAG GCCCACGGCT CAAGTGAATT TGAATACTGC ATTTACAGTG     1200
TAGAGTAACA CATAACATTG TATGCATGGA AACATGGAGG AACAGTATTA CAGTGTCCCTA     1260
CCACTCTAAT CAAGAAAAGA ATTACAGACT CTGATTCTAC AGTGATGATT GAATTCTAAA     1320
AATGGTTATC ATTAGGGCTT TTGATTTATA AAACCTTGGG TACTTATACT AAATTATGGT     1380
AGTTATTCTG CCTTCCAGTT TGCTTGATAT ATTTGTTGAT ATTAAGATTG TTGACTTATA     1440
TTTGAATGG GTTCTAGTGA AAAAGGAATG ATATATTCCT GAAGACATCG ATATACATTT     1500
ATTTACACTC TTGATTCTAC AATGTAGAAA ATGAGGAAAT GCCACAAATT GTATGGTGAT     1560
AAAAGTCACG TGAAACAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA     1620
A                                                                                   1621

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(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

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Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
 1           5           10           15
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
 20           25           30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
 35           40           45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
 50           55           60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
 65           70           75           80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
 85           90           95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
 100          105          110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
 115          120          125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
 130          135          140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Gly Leu Met Cys
 145          150          155          160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
 165          170          175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
 180          185          190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
 195          200          205

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Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
 210 215 220
 Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
 225 230 235 240
 Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
 245 250 255
 Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala
 260 265 270
 Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp
 275 280 285
 Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val
 290 295 300
 His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu
 305 310 315 320
 Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala
 325 330 335
 Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu
 340 345 350
 Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn
 355 360 365
 Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu
 370 375 380

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGCAGGAGGC	TGCCCCAGGG	CCTGAGCGGA	GGCGGGGGCA	GCCTCGCCAG	CGGGGGCCCC	60
GGGCCTGGCC	ATGCCTCACT	GAGCCAGCGC	CTGCGCCTCT	ACCTCGCCGA	CAGCTGGAAC	120
CAGTGCAGAC	TAGTGGCTCT	CACCTGCTTC	CTCCTGGGCG	TGGGCTGCCG	GCTGACCCCG	180
GGTTTGATAC	ACCTGGGCGG	CACCTGCTTC	TGCATCGACT	TCATGGTTTT	CACGGTGCCG	240
CTGCTTCACA	TCTTCACGGT	CAACAAACAG	CTGGGGCCCCA	AGATCGTCAT	CGTGAGCAAG	300
ATGATGAAGG	ACGTGTTCTT	CTTCTCTTTC	TTCTCTCGGC	TGTGGCTGGT	AGCCTATGGC	360
GTGGCCACGG	AGGGGCTCCT	GAGGCCACGG	GACAGTGACT	TCCCAAGTAT	CCTGCGCCGC	420
GTCTTCTACC	GTCCCTACCT	GCAGATCTTC	GGGCAGATTC	CCCAGGAGGA	CATGGACGTG	480
GCCCTCATGG	AGCACAGCAA	CTGCTCGTCG	GAGCCCGGCT	TCTGGGCACA	CCCTCCTGGG	540
GCCCAGGCGG	GCACCTGCGT	CTCCCACTAT	GCCAACTGGC	TGGTGGTGCT	GCTCCTCGTC	600
ATCTTCTGCT	TCGTGGCCAA	CATCCTGCTG	GTCAACTTGC	TCATTGCCAT	GTTCACTTAC	660
ACATTCGGCA	AAGTACAGGG	CAACAGCGAT	CTCTACTGGA	AGGCGCAGCG	TTACCGCCTC	720
ATCCGGGAAT	TCCACTCTCG	GCCCAGCGCTG	GCCCTCGGCT	TTATCGTCAT	CTCCCACTTG	780
CGCCTCCTGC	TCCAGGCAAT	GTGCAGGCGA	CCCCGGAGCC	CCCAGCCGTC	CTCCCGGGCC	840
CTCGAGCATT	TCCGGGTTTA	CCTTTCTAAG	GAAGCCGAGC	GGAAGCTGCT	AACGTGGGAA	900
TCGGTGATCA	AGGAGAACTT	TCTGCTGGCA	CGCGCTAGGG	ACAAGCGGGA	GAGCGACTCC	960
GAGCGTCTGA	AGCGCACGTC	CCAGAAGGTG	GACTTGGCAC	TGAAACAGCT	GGGACACATC	1020
CGCGAGTACG	AACAGCGCCT	GAAAGTGCTG	GAGCGGGAGG	TCCAGCAGTG	TAGCCGCGTC	1080
CTGGGGTGCG	TGGCCGAGGC	CCTGAGCCGC	TCTGCCTTGC	TGCCCCCAGG	TGGGCCGCCA	1140
CCCCCTGACC	TGCCTGGGTC	CAAAGACTGA	GCCCTGCTGG	CGGACTTCAA	GGAGAAGCCC	1200
CCACAGGGGA	TTTTGCTCCT	AGAGTAAGGC	TCATCTGGGC	CTCGGCCCCC	GCACCTGGTG	1260
GCCTTGTCCT	TGAGGTGAGC	CCCATGTCCA	TCTGGGCCAC	TGTCAGGACC	ACCTTTGGGA	1320
GTGTCATCCT	TACAAACCAC	AGCATGCCCC	GCTCCTCCCA	GAACCACTCC	CAGCCTGGGA	1380

GGATCAAGGC	CTGGATCCCG	GGCCGTTATC	CATCTGGAGG	CTGCAGGGTC	CTTGGGGTAA	1440
CAGGGACCAC	AGACCCCTCA	CCACTCACAG	ATTCTCACA	CTGGGAAAT	AAAGCCATTT	1500
CAGAGGAAAA	AAAAAAAAAA	AAAA				1524

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGGAACCAGC	CTGCACGCGC	TGGCTCCGGG	TGACAGCCGC	GCGCCTCGGC	CAGGATCTGA	60
GTGATGAGAC	GTGTCCCCAC	TGAGGTGCC	CACAGCAGCA	GGTGTGAGC	ATGGGCTGAG	120
AAGCTGGACC	GGCACCAAAG	GGCTGGCAGA	AATGGGCGCC	TGGCTGATTC	CTAGGCAGTT	180
GGCGGCAGCA	AGGAGGAGAG	GCCGCAGCTT	CTGGAGCAGA	GCCGAGACGA	AGCAGTTCTG	240
GAGTGCCTGA	ACGGCCCCCT	GAGCCCTACC	CGCCTGGCCC	ACTATGGTCC	AGAGGCTGTG	300
GGTGAGCCGC	CTGCTGCGGC	ACCGGAAAGC	CCAGCTCTTG	CTGGTCAACC	TGCTAACCTT	360
TGGCCTGGAG	GTGTGTTTGG	CCGCAGGCAT	CACCTATGTG	CCGCCTCTGC	TGCTGGAAGT	420
GGGGGTAGAG	GAGAAGTTCA	TGACCATGGT	GCTGGGCATT	GGTCCAGTGC	TGGGCCTGGT	480
CTGTGTCCCG	CTCCTAGGCT	CAGCCAGTGA	CCACTGGCGT	GGACGCTATG	GCCGCCGCCG	540
GCCCTTCATC	TGGGCACGTG	CCTTGGGCAT	CCTGCTGAGC	CTCTTTCTCA	TCCCAAGGGC	600
CGGCTGGCTA	GCAGGGCTGC	TGTGCCCGGA	TCCCAGGCC	CTGGAGCTGG	CACTGCTCAT	660
CCTGGGCGTG	GGGCTGCTGG	ACTTCTGTGG	CCAGGTGTGC	TCACTCCAC	TGGAGGCCCT	720
GCTCTCTGAC	CTCTTCCGGG	ACCCGGACCA	CTGTCGCCAG	GCCTACTCTG	TCTATGCCCT	780
CATGATCAGT	CTTGGGGGCT	GCCTGGGCTA	CCTCCTGCCT	GCCATTGACT	GGGACACCAG	840
TGCCCTGGCC	CCCTACCTGG	GCACCCAGGA	GGAGTGCCTC	TTTGGCCTGC	TCACCCTCAT	900
CTTCCTCACC	TGCGTAGCAG	CCACACTGCT	GGTGGCTGAG	GAGGCAGCGC	TGGGCCCCAC	960
CGAGCCAGCA	GAAGGGCTGT	CGGCCCCCTC	CTGTGCGCCC	CACTGCTGTC	CATGCCGGGC	1020
CCGCTTGGCT	TTCCGGAACC	TGGGCGCCCT	GCTTCCCCGG	CTGCACCAGC	TGTGCTGCCG	1080
CATGCCCCGC	ACCCTGCGCC	GGCTCTTCGT	GGCTGAGCTG	TGCAGCTGGA	TGGCACTCAT	1140
GACCTTCACG	CTGTTTTTACA	CGGATTTTCG	GGGCGAGGGG	CTGTACCAGG	GCGTGCCCAG	1200
AGCTGAGCCG	GGCACCAGAG	CCCGGAGACA	CTATGATGAA	GGCGTTCGGA	TGGGCAGCCT	1260
GGGGCTGTTC	CTGCAGTGCG	CCATCTCCCT	GGTCTTCTCT	CTGGTCATGG	ACCGGCTGGT	1320
GCAGCGATTG	CGCACTATTT	GGCCAGTGTG	GCAGCTTTCC	CTGTGGCTGC		1380
CGGTGCCACA	TGCCTGTCCC	ACAGTGTGGC	CGTGGTGACA	GCTTCAGCCG	CCCTCACCAG	1440
GTTACACCTT	TCAGCCCTGC	AGATCCTGCC	CTACACACTG	GCCTCCCTCT	ACCACCGGGA	1500
GAAGCAGGTG	TTCTTGCCCA	AATACCGAGG	GGACACTGGA	GGTGCTAGCA	GTGAGGACAG	1560
CCTGATGACC	AGCTTCCTGC	CAGGCCCTAA	GCCTGGAGCT	CCCTTCCCTA	ATGGACACGT	1620
GGGTGCTGGA	GGCAGTGGCC	TGCTCCCACC	TCCACCCGCG	CTCTGCGGGG	CCTCTGCCTG	1680
TGATGTCTCC	GTACGTGTGG	TGGTGGGTGA	GCCCACCGAG	GCCAGGGTGG	TTCCGGGGCCG	1740
GGGCATCTGC	CTGGACCTCG	CCATCCTGGA	TAGTGCCTTC	CTGCTGTCCC	AGGTGGCCCC	1800
ATCCCTGTTT	ATGGGCTCCA	TTGTCCAGCT	CAGCCAGTCT	GTCACTGCCT	ATATGGTGTG	1860
TGCCGCAGGC	CTGGGTCTGG	TGCCATTATA	CTTGCTACA	CAGGTAGTAT	TTGACAAGAG	1920
CGACTTGGCC	AAATACTCAG	CGTAGAAAAC	TTCCAGCACA	TTGGGGTGGA	GGGCCTGCCT	1980
CACTGGGTCC	CAGCTCCCCG	CTCCTGTTAG	CCCCATGGGG	CTGCCGGGCT	GGCCGCCAGT	2040
TTCTGTTGCT	GCCAAAGTAA	TGTGGCTCTC	TGCTGCCACC	CTGTGCTGCT	GAGGTGCGTA	2100
GCTGCACAGC	TGGGGGCTGG	GGCGTCCCTC	TCCTCTCTCC	CCAGTCTCTA	GGGCTGCCTG	2160
ACTGGAGGCC	TTCCAAGGGG	GTTTCACTCT	GGACTTATAC	AGGGAGGCCA	GAAGGGCTCC	2220
ATGCACTGGA	ATGCGGGGAC	TCTGCAGGTG	GATTACCCAG	GCTCAGGGTT	AACAGCTAGC	2280
CTCCTAGTTG	AGACACACCT	AGAGAAGGGT	TTTTGGGAGC	TGAATAAACT	CAGTCACCTG	2340
GTTTCCCATC	TCTAAGCCCC	TTAACCTGCA	GCTTCGTTTA	ATGTAGCTCT	TGCATGGGAG	2400
TTTCTAGGAT	GAAACACTCC	TCCATGGGAT	TTGAACATAT	GACTTATTTG	TAGGGGAAGA	2460
GTCCTGAGGG	GCAACACACA	AGAACCAGGT	CCCCCTAGCC	CACAGCACTG	TCTTTTGTCT	2520

GATCCACCCC	CCTCTTACCT	TTTATCAGGA	TGTGGCCTGT	TGGTCCTTCT	GTTGCCATCA	2580
CAGAGACACA	GGCATTTAAA	TATTTAACTT	ATTATTTTAA	CAAAGTAGAA	GGGAATCCAT	2640
TGCTAGCTTT	TCTGTGTTGG	TGTCTAATAT	TTGGGTAGGG	TGGGGGATCC	CCAACAATCA	2700
GGTCCCCTGA	GATAGCTGGT	CATTGGGCTG	ATCATTGCCA	GAATCTTCTT	CTCCTGGGGT	2760
CTGGCCCCC	AAAATGCCTA	ACCCAGGACC	TTGGAAATTC	TACTCATCCC	AAATGATAAT	2820
TCCAAATGCT	GTTACCCAAG	GTTAGGGTGT	TGAAGGAAGG	TAGAGGGTGG	GGCTTCAGGT	2880
CTCAACGGCT	TCCCTAACCA	CCCCCTTCT	CTTGGCCCAG	CCTGGTTCCC	CCCACCTCCA	2940
CTCCCCTCTA	CTCTCTCTAG	GACTGGGCTG	ATGAAGGCAC	TGCCCCAAAAT	TTCCCCCTACC	3000
CCCAACTTTC	CCCTACCCCC	AACTTTCCCC	ACCAGCTCCA	CAACCCTGTT	TGGAGCTACT	3060
GCAGGACCAG	AAGCACAAAG	TGCGGTTTCC	CAAGCCTTTG	TCCATCTCAG	CCCCCAGAGT	3120
ATATCTGTGC	TTGGGGAATC	TCACACAGAA	ACTCAGGAGC	ACCCCTGCC	TGAGCTAAGG	3180
GAGGTCTTAT	CTCTCAGGGG	GGGTTTAAGT	GCCGTTTGCA	ATAATGTCGT	CTTATTTATT	3240
TAGCGGGGTG	AATATTTTAT	ACTGTAAGTG	AGCAATCAGA	GTATAATGTT	TATGGTGACA	3300
AAATTAAAGG	CTTTCTTATA	TGTTTAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	3360
AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAATAA	AAAAAAAAAA		3410

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AGCCAGGCGT	CCCTCTGCCT	GCCCACTCAG	TGGCAACACC	CGGGAGCTGT	TTTGTCTTTT	60
GTGGAGCCTC	AGCAGTTCCC	TCTTTCAGAA	CTCACTGCCA	AGAGCCCTGA	ACAGGAGCCA	120
CCATGCAGTG	CTTCAGCTTC	ATTAAGACCA	TGATGATCCT	CTTCAATTTG	CTCATCTTTT	180
TGTGTGGTGC	AGCCCTGTTG	GCAGTGGGCA	TCTGGGTGTC	AATCGATGGG	GCATCCTTTC	240
TGAAGATCTT	CGGGCCACTG	TCGTCCAGTG	CCATGCAGTT	TGTCAACGTG	GGCTACTTCC	300
TCATCGCAGC	CGGCGTTGTG	GTCTTTGCTC	TTGGTTTCCT	GGGCTGCTAT	GGTGCTAAGA	360
CTGAGAGCAA	GTGTGCCCTC	GTGACGTTCT	TCTTCATCCT	CCTCCTCATC	TTCATTGCTG	420
AGGTTGCAGC	TGCTGTGGTC	GCCTTGGTGT	ACACCACAAT	GGCTGAGCAC	TTCCCTGACGT	480
TGCTGGTAGT	GCCTGCCATC	AAGAAAGATT	ATGGTTCCCA	GGAAGACTTC	ACTCAAGTGT	540
GGAACACCAC	CATGAAAGGG	CTCAAGTGCT	GTGGCTTCAC	CAACTATACG	GATTTTGAGG	600
ACTCACCTTA	CTTCAAAGAG	AACAGTGCTT	TTCCCCCATT	CTGTTGCAAT	GACAACGTCA	660
CCAACACAGC	CAATGAAACC	TGCACCAAGC	AAAAGGCTCA	CGACCAAAAA	GTAGAGGGTT	720
GCTTCAATCA	GCTTTTGTAT	GACATCCGAA	CTAATGCAGT	CACCGTGGGT	GGTGTGGCAG	780
CTGGAATTGG	GGGCCTCGAG	CTGGCTGCCA	TGATTGTGTC	CATGTATCTG	TACTGCAATC	840
TACAATAAGT	CCACTTCTGC	CTCTGCCACT	ACTGCTGCCA	CATGGGAACT	GTGAAGAGGC	900
ACCCTGGCAA	GCAGCAGTGA	TTGGGGGAGG	GGACAGGATC	TAACAATGTC	ACTTGGGCCA	960
GAATGGACCT	GCCCTTTCTG	CTCCAGACTT	GGGGCTAGAT	AGGGACCACT	CCTTTTAGCG	1020
ATGCCTGACT	TTCTTTCCAT	TGGTGGGTGG	ATGGGTGGGG	GGCATTCCAG	AGCCTCTAAG	1080
GTAGCCAGTT	CTGTTGCCCA	TTCCCCCAGT	CTATTAAACC	CTTGATATGC	CCCCTAGGCC	1140
TAGTGGTGAT	CCCAGTGCTC	TACTGGGGGA	TGAGAGAAAG	GCATTTTATA	GCCTGGGCAT	1200
AAGTGAAATC	AGCAGAGCCT	CTGGGTGGAT	GTGTAGAAGG	CACCTCAAAA	TGCATAAACC	1260
TGTTACAATG	TTAAAAAAA	AAAAAAA				1289

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

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Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
 1             5             10             15

Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
      20             25             30

Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
      35             40             45

Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
      50             55             60

Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
      65             70             75             80

Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
      85             90             95

Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
      100            105            110

Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Leu Val Ile Phe
      115            120            125

Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
      130            135            140

Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
      145            150            155            160

Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
      165            170            175

Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln
      180            185            190

Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu
      195            200            205

His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr
      210            215            220

Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp
      225            230            235            240

Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val
      245            250            255

Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg
      260            265            270

Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly
      275            280            285

```

Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly
 290 295 300

Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp
 305 310 315

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 553 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
 1 5 10 15
 Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
 20 25 30
 Ala Ala Gly Ile Thr Tyr Val Pro Leu Leu Leu Glu Val Gly Val
 35 40 45
 Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
 50 55 60
 Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
 65 70 75 80
 Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
 85 90 95
 Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
 100 105 110
 Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
 115 120 125
 Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
 130 135 140
 Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
 145 150 155 160
 Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
 165 170 175
 Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
 180 185 190
 Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
 195 200 205

Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
 210 215 220
 Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
 225 230 235 240
 Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
 245 250 255
 Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
 260 265 270
 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
 275 280 285
 Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
 290 295 300
 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
 305 310 315 320
 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
 325 330 335
 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
 340 345 350
 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
 355 360 365
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
 370 375 380
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
 385 390 395 400
 Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
 405 410 415
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
 420 425 430
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
 435 440 445
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser
 450 455 460
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
 465 470 475 480
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 485 490 495
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
 500 505 510
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
 515 520 525
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp

530

535

540

Lys Ser Asp Leu Ala Lys Tyr Ser Ala
545 550

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
1 5 10 15

Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
20 25 30

Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
35 40 45

Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
50 55 60

Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr
65 70 75 80

Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile
85 90 95

Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr
100 105 110

Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys
115 120 125

Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met
130 135 140

Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp
145 150 155 160

Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn
165 170 175

Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala
180 185 190

His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile
195 200 205

Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly
210 215 220

Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu
 225 230 235 240

Gln

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 366 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GCTCTTTCTC	TCCCCTCCTC	TGAATTTAAT	TCTTTCAACT	TGCAATTTGC	AAGGATTACA	60
CATTTCACTG	TGATGTATAT	TGTGTTGCAA	AAAAAAAAAA	GTGTCTTTGT	TTAAAATTAC	120
TTGGTTTGTG	AATCCATCTT	GCTTTTTCCT	CATTGGAACT	AGTCATTAC	CCATCTCTGA	180
ACTGGTAGAA	AAACATCTGA	AGAGCTAGTC	TATCAGCATC	TGACAGGTGA	ATTGGATGGT	240
TCTCAGAACC	ATTTCAACCA	GACAGCCTGT	TTCTATCCTG	TTTAATAAAT	TAGTTTGGGT	300
TCTCTACATG	CATAACAAAC	CCTGCTCCAA	TCTGTCACAT	AAAAGTCTGT	GACTTGAAGT	360
TTAGTC						366

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 282 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ACAAAGATGA	ACCATTTCCT	ATATTATAGC	AAAATTAAAA	TCTACCCGTA	TTCTAATATT	60
GAGAAATGAG	ATNAAACACA	ATNTTATAAA	GTCTACTTAG	AGAAGATCAA	GTGACCTCAA	120
AGACTTTACT	ATTTTCATAT	TTTAAGACAC	ATGATTTATC	CTATTTTAGT	AACCTGGTTC	180
ATACGTTAAA	CAAAGGATAA	TGTGAACAGC	AGAGAGGATT	TGTTGGCAGA	AAATCTATGT	240
TCAATCTNGA	ACTATCTANA	TCACAGACAT	TTCTATTCTT	TT		282

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

ACACATGTCG CTTCAGTGCC TTCTTAGATG CTTCTGGTCA ACATANAGGA ACAGGGACCA	60
TATTTATCCT CCCTCCTGAA ACAATTGCAA AATAANACAA AATATATGAA ACAATTGCAA	120
AATAAGGCAA AATATATGAA ACAACAGGTC TCGAGATATT GGAAATCAGT CAATGAAGGA	180
TACTGATCCC TGATCACTGT CCTAATGCAG GATGTGGGAA ACAGATGAGG TCACCTCTGT	240
GACTGCCCCA GCTTACTGCC TGTAAGAGAGT TTCTANGCTG CAGTTCAGAC AGGGAGAAAT	300
TGGGT	305

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ACCAAGGTGT NTGAATCTCT GACGTGGGGA TCTCTGATTC CCGCACAATC TGAGTGGA	60
AAATCCTGGG T	71

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ACTCCGGTTG GTGTCAGCAG CACGTGGCAT TGAACATNGC AATGTGGAGC CCAAACCACA	60
GAAAATGGGG TGAAATTGGC CAACTTTCTA TNAACTTATG TTGGCAANTT TGCCACCAAC	120
AGTAAGCTGG CCCTTCTAAT AAAAGAAAAT TGAAAGGTTT CTCACTAANC GGAATTAANT	180
AATGGANTCA AGANACTCCC AGGCCTCAGC GT	212

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

```
ACTCGTTGCA NATCAGGGGC CCCCAGAGT CACCGTTGCA GGAGTCCTTC TGGTCTTGCC 60
CTCCGCCGGC GCAGAACATG CTGGGGTGGT 90
```

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

```
TGTANCGTGA ANACGACAGA NAGGGTTGTC AAAAATGGAG AANCCTTGAA GTCATTTTGA 60
GAATAAGATT TGCTAAAAGA TTTGGGGCTA AAACATGGTT ATTGGGAGAC ATTTCTGAAG 120
ATATNCANGT AAATTANGGA ATGAATTCAT GGTTCCTTTG GGAATTCCTT TACGATNGCC 180
AGCATANACT TCATGTGGGG ATANCAGCTA CCCTTGTA 218
```

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

```
TAGGGGTGTA TGCAACTGTA AGGACAAAAA TTGAGACTCA ACTGGCTTAA CCAATAAAGG 60
CATTTGTTAG CTCATGGAAC AGGAAGTCGG ATGGTGGGGC ATCTTCAGTG CTGCATGAGT 120
CACCACCCCG GCGGGGTCAT CTGTGCCACA GGTCCCTGTT GACAGTGCGG T 171
```

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGTAGCGTGA AGACNACAGA ATGGTGTGTG CTGTGCTATC CAGGAACACA TTTATTATCA 60
TTATCAANTA TTGTGT 76

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

ACCTTTCCCC AAGGCCAATG TCCTGTGTGC TAACTGGCCG GCTGCAGGAC AGCTGCAATT 60
CAATGTGCTG GGTCAATATG AGGGGAGGAG ACTCTAAAAT AGCCAATTTT ATTCTCTTGG 120
TTAAGATTG T 131

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ACTTTATCTA CTGGCTATGA AATAGATGGT GGAAAATTGC GTTACCAACT ATACCACTGG 60
CTTGAAAAAG AGGTGATAGC TCTTCAGAGG ACTTGTGACT TTTGCTCAGA TGCTGAAGAA 120
CTACAGTCTG CATTTGCGAG AAATGAAGAT GAATTTGGAT TAAATGAGGA TGCTGAAGAT 180
TTGCCTCACC AAACAAAAGT GAAACAACTG AGAGAAAATT TTCAGGAAAA AAGACAGTGG 240
CTCTTGAAGT ATCAGTCACT TTTGAGAATG TTTCTTAGTT ACTGCATACT TCATGGATCC 300
CATGGTGGGG GTCTTGCACT TGTAAGAATG GAATTGATTT TGCTTTTGCA AGAATCTCAG 360
CAGGAAACAT CAGAACCCT ATTTTCTAGC CCTCTGTCAG AGCAAACCTC AGTGCCTCTC 420
CTCTTTGCTT GT 432

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ACACAACCTTG AATAGTAAAA TAGAAACTGA GCTGAAATTT CTAATTCAC	60
AGTAAGAATG ATATTTCCCC CCAGGGATCA CCAAATATTT ATAAAAATTT GT	112

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ACCACGAAAC CACAAACAAG ATGGAAGCAT CAATCCACTT GCCAAGCACA GCAG	54
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(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ACCTCATTAG TAATTGTTTT GTTGTTTCAT TTTTTTCTAA TGTCTCCCCT CTACCAGCTC	60
ACCTGAGATA ACAGAATGAA AATGGAAGGA CAGCCAGATT TCTCCTTGC TCTCTGCTCA	120
TTCTCTCTGA AGTCTAGGTT ACCCATTTTG GGGACCCATT ATAGGCAATA AACACAGTTC	180
CCAAAGCATT TGGACAGTTT CTTGTTGTGT TTTAGAATGG TTTTCCTTTT TCTTAGCCTT	240
TTCTTGCAAA AGGCTCACTC AGTCCCTTGC TTGCTCAGTG GACTGGGCTC CCCAGGGCCT	300
AGGCTGCCTT CTTTTCCATG TCC	323

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ACATACATGT GTGTATATTT TTAAATATCA CTTTGTATC ACTCTGACTT TTTAGCATAC	60
TGAAAACACA CTAACATAAT TTNTGTGAAC CATGATCAGA TACAACCCAA ATCATTCATC	120

TAGCACATTC ATCTGTGATA NAAAGATAGG TGAGTTTCAT TTCCTTCACG TTGGCCAATG 180
GATAAACAAA GT 192

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CCCTTTTFTA	TGGAATGAGT	AGACTGTATG	TTTGAANATT	TANCCACAAC	CTCTTTGACA	60
TATAATGACG	CAACAAAAAG	GTGCTGTTTA	GTCTATGGT	TCAGTTTATG	CCCCTGACAA	120
GTTTCCATTG	TGTTTTGCCG	ATCTTCTGGC	TAATCGTGGT	ATCCTCCATG	TTATTAGTAA	180
TTCTGTATTC	CATTTTGTTA	ACGCCTGGTA	GATGTAACCT	GCTANGAGGC	TAACTTTATA	240
CTTATTTAAA	AGCTCTTATT	TTGTGGTCAT	TAAAATGGCA	ATTTATGTGC	AGCACTTTAT	300
TGCAGCAGGA	AGCACGTGTG	GTTTGGTTGT	AAAGCTCTTT	GCTAATCTTA	AAAAGTAATG	360
GG						362

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CTTTTTGAAA	GATCGTGTCC	ACTCCTGTGG	ACATCTTGTT	TTAATGGAGT	TTCCCATGCA	60
GTANGACTGG	TATGGTTGCA	GCTGTCCAGA	TAAAAACATT	TGAAGAGCTC	CAAAATGAGA	120
GTTCTCCCAG	GTTCGCCCTG	CTGCTCCAAG	TCTCAGCAGC	AGCCTCTTTT	AGGAGGCATC	180
TTCTGAACTA	GATTAAGGCA	GCTTGTAAT	CTGATGTGAT	TTGGTTTATT	ATCCAACTAA	240
CTTCCATCTG	TTATCACTGG	AGAAAGCCCA	GACTCCCCAN	GACNGGTACG	GATTGTGGGC	300
ATANAAGGAT	TGGGTGAAGC	TGGCGTTGTG	GT			332

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

ACTTTTGCCA TTTTGTATAT ATAAACAATC TTGGGACATT CTCCTGAAAA CTAGGTGTCC	60
AGTGGCTAAG AGAACTCGAT TTCAAGCAAT TCTGAAAGGA AAACCAGCAT GACACAGAAT	120
CTCAAATTCC CAAACAGGGG CTCTGTGGGA AAAATGAGGG AGGACCTTTG TATCTCGGGT	180
TTTAGCAAGT TAAATGAAN ATGACAGGAA AGGCTTATTT ATCAACAAAG AGAAGAGTTG	240
GGATGCTTCT AAAAAAACT TTGGTAGAGA AAATAGGAAT GCTNAATCCT AGGGAAGCCT	300
GTAACAATCT ACAATTGGTC CA	322

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

ACAAGCCTTC ACAAGTTTAA CTAAATTGGG ATTAATCTTT CTGTANTTAT CTGCATAATT	60
CTTGTTTTTC TTTCCATCTG GTCCTGGGT TGACAATTTG TGGAAACAAC TCTATTGCTA	120
CTATTTAAAA AAAATCACAA ATCTTCCCT TTAAGCTATG TTNAATTCAA ACTATTCCTG	180
CTATTCCTGT TTTGTCAAAG AAATTATATT TTTCAAATA TGTNTATTTG TTTGATGGGT	240
CCCACGAAAC ACTAATAAAA ACCACAGAGA CCAGCCTG	278

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GTTTANAAAA CTTGTTTAGC TCCATAGAGG AAAGAATGTT AAACTTTGTA TTTTAAACA	60
TGATTCTCTG AGGTAAACT TGGTTTCAA ATGTTATTTT TACTTGATT TTGCTTTTGG	120
T	121

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACTTANAACC	ATGCCTAGCA	CATCAGAATC	CCTCAAAGAA	CATCAGTATA	ATCCTATACC	60
ATANCAAGTG	GTGACTGGTT	AAGCGTGCGA	CAAAGGTCAG	CTGGCACATT	ACTTGTGTGC	120
AAACTTGATA	CTTTTGTTC	AAGTAGGAAC	TAGTATACAG	TNCCTAGGAN	TGGTACTCCA	180
GGGTGCCCCC	CAACTCCTGC	AGCCGCTCCT	CTGTGCCAGN	CCCTGNAAGG	AACTTTCGCT	240
CCACCTCAAT	CAAGCCCTGG	GCCATGCTAC	CTGCAATTGG	CTGAACAAAC	GTTTGCTGAG	300
TTCCCAAGGA	TGCAAAGCCT	GGTGCTCAAC	TCCTGGGGCG	TCAACTCAGT		350

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

TGTACCGTGA	AGACGACAGA	AGTTGCATGG	CAGGGACAGG	GCAGGGCCGA	GGCCAGGGTT	60
GCTGTGATTG	TATCCGAATA	NTCCTCGTGA	GAAAAGATAA	TGAGATGACG	TGAGCAGCCT	120
GCAGACTTGT	GTCTGCCTTC	AANAAGCCAG	ACAGGAAGGC	CCTGCCTGCC	TTGGCTCTGA	180
CCTGGCGGCC	AGCCAGCCAG	CCACAGGTGG	GCTTCTTCCT	TTTGTGGTGA	CAACNCCAAG	240
AAAAGTGCAG	AGGCCCAGGG	TCAGGTGTNA	GTGGGTANGT	GACCATAAAA	CACCAGGTGC	300
TCCAGGAAC	CCGGGCAAAG	GCCATCCCCA	CCTACAGCCA	GCATGCCCAC	TGGCGTGATG	360
GGTGACAGANG	GATGAAGCAG	CCAGNTGTTC	TGCTGTGGT			399

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 165 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACTGGTGTGG	TNGGGGGTGA	TGCTGGTGGT	ANAAGTTGAN	GTGACTTCAN	GATGGTGTGT	60
GGAGGAAGTG	TGTGAACGTA	GGGATGTAGA	NGTTTGGCC	GTGCTAAATG	AGCTTCGGGA	120
TTGGCTGGTC	CCACTGGTGG	TCACTGTCAT	TGGTGGGGTT	CCTGT		165

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

ACTCACTGGA	ATGCCACATT	CACAACAGAA	TCAGAGGTCT	GTGAAAACAT	TAATGGCTCC	60
TTAACTTCTC	CAGTAAGAAT	CAGGGACTTG	AAATGGAAAC	GTTAACAGCC	ACATGCCCAA	120
TGCTGGGCAG	TCTCCCATGC	CTTCCACAGT	GAAAGGGCTT	GAGAAAAATC	ACATCCAATG	180
TCATGTGTTT	CCAGCCACAC	CAAAAGGTGC	TTGGGGTGGA	GGGCTGGGGG	CATANANGGT	240
CANGCCTCAG	GAAGCCTCAA	GTTCCATTCA	GCTTTGCCAC	TGTACATTCC	CCATNTTTAA	300
AAAAACTGAT	GCCTTTTTTT	TTTTTTTTTG	TAAAATTG			338

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGGAATCTTG	GTTTTTGGCA	TCTGGTTTGC	CTATAGCCGA	GGCCACTTTG	ACAGAACAAA	60
GAAAGGGACT	TCGAGTAAGA	AGGTGATTTA	CAGCCAGCCT	AGTGCCCGAA	GTGAAGGAGA	120
ATTCAAACAG	ACCTCGTCAT	TCCTGGTGTG	AGCCTGGTCG	GCTCACC GCC	TATCATCTGC	180
ATTTGCCTTA	CTCAGGTGCT	ACCGGACTCT	GGCCCTGAT	GTCTGTAGTT	TCACAGGATG	240
CCTTATTTGT	CTTCTACACC	CCACAGGGCC	CCCTACTTCT	TCGGATGTGT	TTTTAATAAT	300
GTCAGCTATG	TGCCCCATCC	TCCTTCATGC	CCTCCCTCCC	TTTCCTACCA	CTGCTGAGTG	360
GCCTGGAAGT	TGTTTAAAGT	GT				382

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ACCAANCTT	CTTCTGTTG	TGTTNGATTT	TACTATAGGG	GTTTNGCTTN	TTCTAAANAT	60
ACTTTTCATT	TAACANCTTT	TGTTAAGTGT	CAGGCTGCAC	TTTGCTCCAT	ANAATTATTG	120
TTTTACATT	TCAACTTGTA	TGTGTTTGTC	TCTTANAGCA	TTGGTGAAAT	CACATATTTT	180
ATATTCAGCA	TAAAGGAGAA					200

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

ACTTTATTTT CAAAACACTC ATATGTTGCA AAAACACAT AGAAAAATAA AGTTTGGTGG	60
GGGTGCTGAC TAAACTTCAA GTCACAGACT TTTATGTGAC AGATTGGAGC AGGTTTGT	120
ATGCATGTAG AGAACCCAAA CTAATTTATT AAACAGGATA GAAACAGGCT GTCTGGGTGA	180
AATGGTTCTG AGAACCATCC AATTCACCTG TCAGATGCTG ATANACTAGC TCTTCAGATG	240
TTTTTCTACC AGTTCAGAGA TNGGTTAATG ACTANTTCCA ATGGGGAAAA AGCAAGATGG	300
ATTCACAAAC CAAGTAATTT TAAACAAAGA CACTT	335

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

ACCAGGTAA TATTGCCACA TATATCCTTT CCAATTGCGG GCTAAACAGA CGTGATTTTA	60
GGGTTGTTTA AAGACAACCC AGCTTAATAT CAAGAGAAAT TGTGACCTTT CATGGAGTAT	120
CTGATGGAGA AAACACTGAG TTTTGACAAA TCTTATTTTA TTCAGATAGC AGTCTGATCA	180
CACATGGTCC AACAACACTC AAATAATAAA TCAAATATNA TCAGATGTTA AAGATTGGTC	240
TTCAAACATC ATAGCCAATG ATGCCCCGCT TGCCTATAAT CTCTCCGACA TAAAACCACA	300
TCAACACCTC AGTGGCCACC AAACCATCA GCACAGCTTC CTTAACTGTG AGCTGTTTGA	360
AGTACCAAGT CTGAGCACTA TTGACTATNT TTTTCANGCT CTGAATAGCT CTAGGGATCT	420
CAGCANGGGT GGGAGGAACC AGCTCAACCT TGGCGTANT	459

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

ACATTTCTT CCACCAAGTC AGGACTCCTG GCTTCTGTGG GAGTTCTTAT CACCTGAGGG	60
AAATCCAAAC AGTCTCTCCT AGAAAGGAAT AGTGTCACCA ACCCCACCCA TCTCCCTGAG	120
ACCATCCGAC TTCCCTGTGT	140

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACTTCAGTAA CAACATACAA TAACAACATT AAGTGTATAT TGCCATCTTT GTCATTTTCT	60
ATCTATACCA CTCTCCCTTC TGAAAACAAN AATCACTANC CAATCACTTA TACAAATTG	120
AGGCAATTAA TCCATATTTG TTTTCAATAA GGAAAAAAG ATGT	164

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

ACGTAGACCA TCCAACCTTG TATTTGTAAT GGCAAACATC CAGNAGCAAT TCCTAAACAA	60
ACTGGAGGGT ATTTATACCC AATTATCCCA TTCATTAACA TGCCCTCCTC CTCAGGCTAT	120
GCAGGACAGC TATCATAAGT CGGCCAGGC ATCCAGATAC TACCATTTGT ATAAACTCA	180
GTAGGGGAGT CCATCCAAGT GACAGGTCTA ATCAAAGGAG GAAATGGAAC ATAAGCCCAG	240
TAGTAAAATN TTGCTTAGCT GAAACAGCCA CAAAAGACTT ACCGCCGTGG TGATTACCAT	300
CAA	303

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

ACTGCAGCTC AATTAGAAGT GGTCTCTGAC TTTCATCANC TTCTCCCTGG GCTCCATGAC	60
ACTGGCCTGG AGTGACTCAT TGCTCTGGTT GGTGAGAGA GTCCTTTTGC CAACAGGCCT	120
CCAAGTCAGG GCTGGGATT TTTTCCTTTC CACATTCTAG CAACAATATG CTGGCCACTT	180
CCTGAACAGG GAGGGTGGGA GGAGCCAGCA TGAACAAGC TGCCACTTTC TAAAGTAGCC	240
AGACTTGCCC CTGGGCCTGT CACACCTACT GATGACCTTC TGTGCCTGCA GGATGGAATG	300
TAGGGGTGAG CTGTGTGACT CTATGGT	327

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ACATTGTTTT TTGAGATAA AGCATTGANA GAGCTCTCCT TAACGTGACA CAATGGAAGG	60
ACTGGAACAC ATACCCACAT CTTGTTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT	120
ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTT	173

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

ACAACCACTT TATCTCATCG AATTTTAAAC CCAAATCAC TCACTGTGCC TTTCTATCCT	60
ATGGGATATA TTATTTGATG CTCCATTTCA TCACACATAT ATGAATAATA CACTCATACT	120
GCCCTACTAC CTGCTGCAAT AATCACATTC CCTTCCTGTC CTGACCCTGA AGCCATTGGG	180
GTGGTCCTAG TGGCCATCAG TCCANGCCTG CACCTTGAGC CCTTGAGCTC CATTGCTCAC	240
NCCANCCAC CTCACCGACC CCATCCTCTT ACACAGCTAC CTCCTTGCTC TCTAACCCCA	300
TAGATTATNT CCAAATTCAG TCAATTAAGT TACTATTAAC ACTCTACCCG ACATGTCCAG	360
CACCACTGGT AAGCCTTCTC CAGCCAACAC ACACACACAC ACACNCACAC ACACACATAT	420
CCAGGCACAG GCTACCTCAT CTTACAATC ACCCCTTTAA TTACCATGCT ATGGTG	477

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 207 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ACAGTTGTAT TATAATATCA AGAAATAAAC TTGCAATGAG AGCATTTAAG AGGGAAGAAC	60
TAACGTATTT TAGAGAGCCA AGGAAGGTTT CTGTGGGGAG TGGGATGTAA GGTGGGGCCT	120

GATGATAAAT AAGAGTCAGC CAGGTAAGTG GGTGGTGTGG TATGGGCACA GTGAAGAACA 180
TTTCAGGCAG AGGGAACAGC AGTGAAA 207

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

ACCTTGATTT CATTGCTGCT CTGATGGAAA CCCAACTATC TAATTTAGCT AAAACATGGG 60
CACTTAAATG TGGTCAGTGT TTGGACTTGT TAACTANTGG CATCTTTGGG T 111

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 196 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AGCGCGGCAG GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTTGATAAC 60
AGCAAGATGG CTTTGAAGTC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAAACCAT 120
GGATACCAAC CGGAAAACCC CTATCCCGCA CAGCCCACTG TGGTCCCCAC TGTCTACGAG 180
GTGCATCCGG CTCAGT 196

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

ACAGCACTTT CACATGTAAG AAGGGAGAAA TTCCTAAATG TAGGAGAAAG ATAACAGAAC 60
CTTCCCCTTT TCATCTAGTG GTGGAAACCT GATGCTTTAT GTTGACAGGA ATAGAACCAG 120
GAGGGAGTTT GT 132

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

ACAANACCCA NGANAGGCCA CTGGCCGTGG TGTCATGGCC TCCAAACATG AAAGTGTGAG	60
CTTCTGCTCT TATGTCCTCA TCTGACAACT CTTTACCATT TTTATCCTCG CTCAGCAGGA	120
GCACATCAAT AAAGTCCAAA GTCTTGGACT TGGCCTTGGC TTGGAGGAAG TCATCAACAC	180
CCTGGCTAGT GAGGGTGCGG CGCCGCTCCT GGATGACGGC ATCTGTGAAG TCGTGCACCA	240
GTCTGCAGGC CCTGTGGAAG CGCCGTCCAC ACGGAGTNAG GAATT	285

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ACCACAGTCC TGTGGGCCA GGGCTTCATG ACCCTTCTG TGAAAAGCCA TATTATCACC	60
ACCCCAAATT TTTCTTAAA TATCTTAAAC TGAAGGGGTC AGCCTCTTGA CTGCAAAGAC	120
CCTAAGCCGG TTACACAGCT AACTCCCACT GGCCCTGATT TGTGAAATTG CTGCTGCCTG	180
ATTGGCACAG GAGTCGAAGG TGTTACAGCTC CCCTCCTCCG TGGAACGAGA CTCTGATTG	240
AGTTTCACAA ATTCTCGGGC CACCTCGTCA TTGCTCCTCT GAAATAAAAT CCGGAGAATG	300
GTGAGGCCTG TCTCATCCAT ATGGATCTTC CGG	333

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

ACTGGAAATA ATAAAACCCA CATCACAGTG TTGTGTCAAA GATCATCAGG GCATGGATGG	60
GAAAGTGCTT TGGGAAGTGT AAAGTGCCTA ACACATGATC GATGATTTT GTTATAATAT	120
TTGAATCAG GTGCATACAA ACTCTCCTGC CTGCTCCTCC TGGGCCCCAG CCCCAGCCCC	180
ATCACAGCTC ACTGCTCTGT TCATCCAGGC CCAGCATGTA GTGGCTGATT CTTCTTGGCT	240

GCTTTTAGCC TCCANAAGTT TCTCTGAAGC CAACCAAACC TCTANGTGTA AGGCATGCTG 300
GCCCTGGT 308

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 295 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

ACCTTGCTCG GTGCTTGGA CATATTAGGA ACTCAAATA TGAGATGATA ACAGTGCCTA 60
 TTATTGATTA CTGAGAGAAC TGTTAGACAT TTAGTTGAAG ATTTTCTACA CAGGAACTGA 120
 GAATAGGAGA TTATGTTTGG CCCTCATATT CTCTCCTATC CTCCTTGCCT CATTCTATGT 180
 CTAATATATT CTCAATCAA TAAGGTTAGC ATAATCAGGA AATCGACCAA ATACCAATAT 240
 AAAACCAGAT GTCTATCCTT AAGATTTTCA AATAGAAAAC AAATTAACAG ACTAT 295

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ACAAGTTTAA ATAGTGCTGT CACTGTGCAT GTGCTGAAAT GTGAAATCCA CCACATTTCT 60
 GAAGAGCAAA ACAAAATTCTG TCATGTAATC TCTATCTTGG GTCGTGGGTA TATCTGTCCC 120
 CTTAGT 126

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 442 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ACCCACTGGT CTTGGAAACA CCCATCCTTA ATACGATGAT TTTTCTGTCTG TGTGAAAATG 60
 AANCCAGCAG GCTGCCCCTA GTCAGTCCTT CCTTCCAGAG AAAAAGAGAT TTGAGAAAGT 120
 GCCTGGGTAA TTCACCATTA ATTTCCTCCC CCAAACCTCTC TGAGTCTTCC CTTAATATTT 180

100

CTGGTGGTTC	TGACCAAGC	AGGTCATGGT	TTGTTGAGCA	TTTGGGATCC	CAGTGAAGTA	240
NATGTTTGTA	GCCTTGCATA	CTTAGCCCTT	CCCACGCACA	AACGGAGTGG	CAGAGTGGTG	300
CCAACCCTGT	TTTCCAGTC	CACGTAGACA	GATTACAGT	GCGGAATTCT	GGAAGCTGGA	360
NACAGACGGG	CTCTTGCAG	AGCCGGGACT	CTGAGANGGA	CATGAGGGCC	TCTGCCTCTG	420
TGTTCAATTCT	CTGATGTCCT	GT				442

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

ACTTCCAGGT	AACGTTGTTG	TTTCCGTTGA	GCCTGAACTG	ATGGGTGACG	TTGTAGGTTC	60
TCCAACAAGA	ACTGAGGTTG	CAGAGCGGGT	AGGGAAGAGT	GCTGTTCCAG	TTGCACCTGG	120
GCTGCTGTGG	ACTGTTGTTG	ATTCTCACT	ACGGCCCAAG	GTTGTGGAAC	TGGCANAAAG	180
GTGTGTTGTT	GGANTTGAGC	TCGGGCGGCT	GTGGTAGGTT	GTGGGCTCTT	CAACAGGGGC	240
TGCTGTGGTG	CCGGGANGTG	AANGTGTGT	GTCACTTGAG	CTTGCCAGC	TCTGGAAAGT	300
ANTANATTCT	TCCTGAAGGC	CAGCGCTTGT	GGAGCTGGCA	NGGGTCANTG	TTGTGTGTAA	360
CGAACCAGTG	CTGCTGTGGG	TGGGTGTANA	TCCTCCACAA	AGCCTGAAGT	TATGGTGTCTN	420
TCAGGTAANA	ATGTGGTTTC	AGTGTCCCTG	GGCNGCTGTG	GAAGGTTGTA	NATTGTCACC	480
AAGGGAATAA	GCTGTGGT					498

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ACCTGCATCC	AGCTTCCCTG	CCAAACTCAC	AAGGAGACAT	CAACCTCTAG	ACAGGGAAC	60
AGCTTCAGGA	TACTTCCAGG	AGACAGAGCC	ACCAGCAGCA	AAACAAATAT	TCCCATGCCT	120
GGAGCATGGC	ATAGAGGAAG	CTGANAAATG	TGGGGTCTGA	GGAAGCCATT	TGAGTCTGGC	180
CACTAGACAT	CTCATCAGCC	ACTTGTGTGA	AGAGATGCCC	CATGACCCCA	GATGCCTCTC	240
CCACCCTTAC	CTCCATCTCA	CACACTTGAG	CTTCCACTC	TGTATAATT	TAACATCCTG	300
GAGAAAAATG	GCAGTTTGAC	CGAACCTGTT	CACAACGGTA	GAGGCTGATT	TCTAACGAAA	360
CTTGTAAGAT	GAAGCCTGGA					380

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

ACTCCACATC CCCTCTGAGC AGGCGGTTGT CGTTCAAGGT GTATTTGGCC TTGCCTGTCA	60
CACTGTCCAC TGGCCCCTTA TCCACTTGGT GCTTAATCCC TCGAAAGAGC ATGT	114

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

ACTTTCTGAA TCGAATCAAA TGATACTTAG TGTAGTTTAA ATATCCTCAT ATATATCAAA	60
GTTTTACTAC TCTGATAATT TTGTAAACCA GGTAACCAGA ACATCCAGTC ATACAGCTTT	120
TGGTGATATA TAACTTGGCA ATAACCCAGT CTGGTGATAC ATAAACTAC TCACTGT	177

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CATTTATACA GACAGGCGTG AAGACATTCA CGACAAAAC GCGAAATTCT ATCCCGTGAC	60
CANAGAAGGC AGCTACGGCT ACTCCTACAT CTTGGCGTGG GTGGCCTTCG CCTGCACCTT	120
CATCAGCGGC ATGATGT	137

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CTTATCACAA TGAATGTTCT CCTGGGCAGC GTTGTGATCT TTGCCACCTT CGTGACTTTA	60
TGCAATGCAT CATGCTATTT CATACTAAT GAGGGAGTTC CAGGAGATTC AACCAGGAAA	120
TGCATGGATC TCAAAGGAAA CAAACACCCA ATAACTCGG AGTGGCAGAC TGACAACTGT	180
GAGACATGCA CTTGCTACGA AACAGAAATT TCATGTTGCA CCCTTGTTTC TACACCTGTG	240
GGTTATGACA AAGACAACTG CCAAAGAATC TTCAAGAAGG AGGACTGCAA GTATATCGTG	300
GTGGAGAAGA AGGACCCAAA AAAGACCTGT TCTGTCACTG AATGGATAAT CTAATGTGCT	360
TCTAGTAGGC ACAGGGCTCC CAGGCCAGGC CTCATTCTCC TCTGGCCTCT AATAGTCAAT	420
GATTGTGTAG CCATGCCTAT CAGTAAAAAG ATNTTTGAGC AAACACTTT	469

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

ACAGTTTTTT ATANATATCG ACATGCGCG CACTTGTGTT CAGTTTCATA AAGCTGGTGG	60
ATCCGCTGTC ATCCACTATT CCTTGGCTAG AGTAAAAATT ATTCTTATAG CCCATGTCCC	120
TGCAGGCCGC CCGCCCGTAG TTCTCGTTCC AGTCGTCTTG GCACACAGGG TGCCAGGACT	180
TCCTCTGAGA TGAGT	195

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

ACATCTTAGT AGTGTGGCAC ATCAGGGGGC CATCAGGGTC ACAGTCACTC ATAGCCTCGC	60
CGAGGTCGGA GTCCACACCA CCGGTGTAGG TGTGCTCAAT CTTGGGCTTG GCGCCACCT	120
TTGGAGAAGG GATATGCTGC ACACACATGT CCACAAAGCC TGTGAAGTCG CCAAAGAATT	180
TTTGACAGAC AGCCTGAGCA AGGGGCGGAT GTTCAGCTTC AGTCCTCCT TCGTCAGGTG	240
GATGCCAACC TCGTCTANGG TCCGTGGGAA GCTGGTGTCC ACNTCACCTA CAACCTGGGC	300
GANGATCTTA TAAAGAGGCT CCNAGATAAA CTCACGAAA CTTCTCTGGG AGCTGCTAGT	360
NGGGGCCTTT TTGGTGAAC TTC	383

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

ACAGAGCCAG ACCTTGGCCA TAAATGAANC AGAGATTAAG ACTAAACCCC AAGTCGANAT	60
TGGAGCAGAA ACTGGAGCAA GAAGTGGGCC TGGGGCTGAA GTAGAGACCA AGGCCACTGC	120
TATANCCATA CACAGAGCCA ACTCTCAGGC CAAGGCNATG GTTGGGGCAG ANCCAGAGAC	180
TCAATCTGAN TCCAAAGTGG TGGCTGGAAC ACTGGTCATG ACANAGGCAG TGACTCTGAC	240
TGANGTC	247

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

ACTTCTAAGT TTTCTAGAAG TGGAAGGATT GTANTCATCC TGAAAATGGG TTTACTTCAA	60
AATCCCTCAN CCTGTCTT CACNACTGTC TATACTGANA GTGTCATGTT TCCACAAAGG	120
GCTGACACCT GAGCCTGNAT TTTCACTCAT CCCTGAGAAG CCCTTTCCAG TAGGGTGGGC	180
AATTCCCAAC TTCCTTGCCA CAAGCTTCCC AGGCTTTCTC CCCTGGAAAA CTCCAGCTTG	240
AGTCCCAGAT ACACTCATGG GCTGCCCTGG GCA	273

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

ACAGCCTTGG CTTCCCCAAA CTCCACAGTC TCAGTGCAGA AAGATCATCT TCCAGCAGTC	60
AGCTCAGACC AGGGTCAAAG GATGTGACAT CAACAGTTTC TGGTTTCAGA ACAGGTTCTA	120
CTACTGTCAA ATGACCCCCC ATACTTCCTC AAAGGCTGTG GTAAGTTTGT CACAGGTGAG	180
GGCAGCAGAA AGGGGGTANT TACTGATGGA CACCATCTTC TCTGTATACT CCACACTGAC	240
CTTGCCATGG GCAAAGGCC CTACCACAAA AACAATAGGA TCACTGCTGG GCACCAGCTC	300
ACGCACATCA CTGACAACCG GGATGGAAAA AGAANTGCCA ACTTTCATAC ATCCAACCTGG	360
AAAGTGATCT GATACTGGAT TCTTAATTAC CTTCAAAGC TTCTGGGGGC CATCAGCTGC	420
TCGAACACTG A	431

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

ACCTGTGGGC TGGGCTGTTA TGCCTGTGCC GGCTGCTGAA AGGGAGTTCA GAGGTGGAGC	60
TCAAGGAGCT CTGCAGGCAT TTTGCCAANC CTCTCCANAG CANAGGGAGC AACCTACACT	120
CCCCGCTAGA AAGACACCAG ATTGGAGTCC TGGGAGGGGG AGTTGGGGTG GGCATTTGAT	180
GTATACTTGT CACCTGAATG AANGAGCCAG AGAGGAANGA GACGAANATG ANATTGGCCT	240
TCAAAGCTAG GGGTCTGGCA GGTGGA	266

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GGCAGCCAAA TCATAACGG CGAGGACTGC AGCCCGCACT CGCAGCCCTG GCAGGCGGCA	60
CTGGTCATGG AAAACGAATT GTTCTGCTCG GGCGTCTTGG TGCATCCGCA GTGGGTGCTG	120
TCAGCCGCAC ACTGTTTCCA GAAGTGAGTG CAGAGCTCCT ACACCATCGG GCTGGGCCTG	180
CACAGTCTTG AGGCCGACCA AGAGCCAGGG AGCCAGATGG TGGAGGCCAG CCTCTCCGTA	240
CGGCACCCAG AGTACAACAG ACCCTTGCTC GCTAACGACC TCATGCTCAT CAAGTTGGAC	300
GAATCCGTGT CCGAGTCTGA CACCATCCGG AGCATCAGCA TTGCTTCGCA GTGCCCTACC	360
GCGGGGAAGT CTTGCCTCGT TTCTGGCTGG GGTCTGCTGG CGAACGGCAG AATGCCTACC	420
GTGCTGCAGT GCGTGAACGT GTCGGTGGTG TCTGAGGAGG TCTGCAGTAA GCTCTATGAC	480
CCGCTGTACC ACCCCAGCAT GTTCTGCGCC GGCGGAGGGC AAGACCAGAA GGACTCCTGC	540
AACGGTGACT CTGGGGGGCC CCTGATCTGC AACCGGTACT TGCAGGGCCT TGTGTCTTTC	600
GGAAAAGCCC CGTGTGGCCA AGTTGGCGTG CCAGGTGTCT ACACCAACCT CTGCAAATTC	660
ACTGAGTGGA TAGAGAAAAC CGTCCAGGCC AGTTAACTCT GGGGACTGGG AACCCATGAA	720
CCCTCAGGCC CAGGAGTCCA GGCCCCCAGC CCCTCCTCCC TCAAACCAAG GGTACAGATC	780
CCCAGCCCCT CCTCCCTCAG ACCCAGGAGT CCAGACCCCC CAGCCCCTCC TCCCTCAGAC	840
CCAGGAGTCC AGCCCCTCCT CCCTCAGACC CAGGAGTCCA GACCCCCCAG CCCCTCCTCC	900
CTCAGACCCA GGGGTCCAGG CCCCCAACCC CTCCTCCCTC AGACTCAGAG GTCCAAGCCC	960
CCAACCCNTC ATTCCCCAGA CCCAGAGGTC CAGGTCCCAG CCCCTCNTCC CTCAGACCCA	1020
GCGGTCCAAT GCCACCTAGA CTNTCCCTGT ACACAGTGCC CCCTTGTTGGC ACGTTGACCC	1080
AACCTTACCA GTTGGTTTTT CATTTTTNGT CCCTTTCCCC TAGATCCAGA AATAAAGTTT	1140
AAGAGAAGNG CAAAAA AAAA AAAAAA AAAAAA AAAAAA	1200
	1248

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

```

Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro
1           5           10           15
Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
          20           25           30
Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
          35           40           45
Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly
          50           55           60
Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu
65           70           75           80
Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe
          85           90           95
Cys Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser
          100          105          110
Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe
          115          120          125
Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn
          130          135          140
Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
          145          150          155

```

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

```

GGCAGCCCCGC ACTGCAGCC CTGGCAGGCG GCACTGGTCA TGGAAAACGA ATTGTTCTGC      60
TCGGGCGTCC TGGTGCATCC GCAGTGGGTG CTGTCAGCCG CACACTGTTT CCAGAACTCC      120
TACACCATCG GGCTGGGCCT GCACAGTCTT GAGGCCGACC AAGAGCCAGG GAGCCAGATG      180
GTGGAGGCCA GCCTCTCGT ACGGCACCCA GAGTACAACA GACCCTTGCT CGCTAACGAC      240

```

CTCATGCTCA	TCAAGTTGGA	CGAATCCGTG	TCCGAGTCTG	ACACCATCCG	GAGCATCAGC	300
ATTGCTTCGC	AGTGCCCTAC	CGCGGGGAAC	TCTTGCCTCG	TTTCTGGCTG	GGGTCTGCTG	360
GCGAACGGTG	AGCTCACGGG	TGTGTGTCTG	CCCTCTTCAA	GGAGGTCTCT	TGCCCAGTCG	420
CGGGGGCTGA	CCAGAGCTC	TGCGTCCCAG	GCAGAATGCC	TACCGTGCTG	CAGTGCGTGA	480
ACGTGTCTGGT	GGTGTCTGAG	GAGGTCTGCA	GTAAGCTCTA	TGACCCGCTG	TACCACCCCA	540
GCATGTTCTG	CGCCGGCGGA	GGGCAAGACC	AGAAGGACTC	CTGCAACGGT	GACTCTGGGG	600
GGCCCCTGAT	CTGCAACGGG	TACTTGCAGG	GCCTTGTGTC	TTTCGGAAAA	GCCCCGTGTG	660
GCCAAGTTGG	CGTGCCAGGT	GTCTACACCA	ACCTCTGCAA	ATTCACTGAG	TGGATAGAGA	720
AAACCGTCCA	GGCCAGTTAA	CTCTGGGGAC	TGGGAACCCA	TGAAATTGAC	CCCCAAATAC	780
ATCCTGCGGA	AGGAATTCAG	GAATATCTGT	TCCCAGCCCC	TCCTCCCTCA	GGCCCAGGAG	840
TCCAGGCCCC	CAGCCCTCC	TCCCTCAAAC	CAAGGGTACA	GATCCCCAGC	CCCTCCTCCC	900
TCAGACCCAG	GAGTCCAGAC	CCCCCAGCCC	CTCCTCCCTC	AGACCCAGGA	GTCCAGCCCC	960
TCCTCCNTCA	GACCCAGGAG	TCCAGACCCC	CCAGCCCCTC	CTCCCTCAGA	CCCAGGGGTT	1020
GAGGCCCCCA	ACCCCTCCTC	CTTCAGAGTC	AGAGGTCCAA	GCCCCCAACC	CCTCGTTCCC	1080
CAGACCCAGA	GGTNNAGGTC	CCAGCCCCTC	TTCCNTCAGA	CCCAGNGGTC	CAATGCCACC	1140
TAGATTTTCC	CTGNACACAG	TGCCCCCTTG	TGGNANGTTG	ACCCAACCTT	ACCAGTTGGT	1200
TTTTCAATTT	TNGTCCCTTT	CCCCTAGATC	CAGAAATAAA	GTTTAAGAGA	NGNGCAAAAA	1260
AAAAA						1265

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GGTCAGCCGC	ACACTGTTTC	CAGAAGTGAG	TGCAGAGCTC	CTACACCATC	GGGCTGGGCC	60
TGCACAGTCT	TGAGGCCGAC	CAAGAGCCAG	GGAGCCAGAT	GGTGGAGGCC	AGCCTCTCCG	120
TACGGCACCC	AGAGTACAAC	AGACCCTTGC	TCGCTAACGA	CCTCATGCTC	ATCAAGTTGG	180
ACGAATCCGT	GTCCGAGTCT	GACACCATCC	GGAGCATCAG	CATTGCTTCG	CAGTGCCCTA	240
CCGCGGGGAA	CTCTTGCCCT	GTTTCTGGCT	GGGGTCTGCT	GGCGAACGGT	GAGCTCACGG	300
GTGTGTGTCT	GCCCTCTTCA	AGGAGGTCCT	CTGCCCAGTC	GCGGGGGCTG	ACCCAGAGCT	360
CTGCGTCCCA	GGCAGAATGC	CTACCGTGCT	GCAGTGCGTG	AACGTGTCTG	TGGTGTCTGA	420
NGAGGTCTGC	ANTAAGCTCT	ATGACCCGCT	GTACCACCCC	ANCATGTTCT	GCGCCGGCGG	480
AGGGCAAGAC	CAGAAGGACT	CCTGCAACGT	GAGAGAGGGG	AAAGGGGAGG	GCAGGCCGACT	540
CAGGGAAGGG	TGGAGAAGGG	GGAGACAGAG	ACACACAGGG	CCGCATGGCG	AGATGCAGAG	600
ATGGAGAGAC	ACACAGGGAG	ACAGTGACAA	CTAGAGAGAG	AAACTGAGAG	AAACAGAGAA	660
ATAAACACAG	GAATAAAGAG	AAGCAAAGGA	AGAGAGAAAC	AGAAACAGAC	ATGGGGAGGC	720
AGAAACACAC	ACACATAGAA	ATGCAGTTGA	CCTTCCAACA	GCATGGGGCC	TGAGGGCGGT	780
GACCTCCACC	CAATAGAAAA	TCCTCTTATA	ACTTTTGACT	CCCCAAAAAC	CTGACTAGAA	840
ATAGCCTACT	GTTGACGGGG	AGCCTTACCA	ATAACATAAA	TAGTCGATTT	ATGCATACGT	900
TTTATGCATT	CATGATATAC	CTTGTGTGGA	ATTTTGTGAT	ATTCTAAGC	TACACAGTTC	960
GTCTGTGAAT	TTTTTTAAAT	TGTTGCAACT	CTCCTAAAAT	TTTTCTGATG	TGTTTATTGA	1020
AAAAATCCAA	GTATAAGTGG	ACTTGTGCAT	TCAAACCAGG	GTTGTTCAAG	GGTCAACTGT	1080
GTACCCAGAG	GGAAACAGTG	ACACAGATTC	ATAGAGGTGA	AACACGAAGA	GAAACAGGAA	1140
AAATCAAGAC	TCTACAAAGA	GGCTGGGCAG	GGTGCTCAT	GCCTGTAATC	CCAGCACTTT	1200
GGGAGGCGAG	GCAGGCAGAT	CACCTGAGGT	AAGGAGTTCA	AGACCAGCCT	GGCCAAAATG	1260
GTGAAATCCT	GTCTGTACTA	AAAATACAAA	AGTTAGCTGG	ATATGGTGGC	AGGCGCCTGT	1320
AATCCCAGCT	ACTTGGGAGG	CTGAGGCAGG	AGAATTGCTT	GAATATGGGA	GGCAGAGGTT	1380
GAAGTGAGTT	GAGATCACAC	CACTATACTC	CAGCTGGGGC	AACAGAGTAA	GACTCTGTCT	1440
CAAAAAAAAA	AAAAAAAAAA					1459

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1167 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

```

GCGCAGCCCT GGCAGGCGGC ACTGGTCATG GAAAACGAAT TGTTCGTCTC GGGCGTCTCTG      60
GTGCATCCGC AGTGGGTGCT GTCAGCCGCA CACTGTTTCC AGAACTCCTA CACCATCGGG      120
CTGGGCGCTG ACAGTCTTGA GGCCGACCAA GAGCCAGGGA GCCAGATGGT GGAGGCCAGC      180
CTCTCCGTAC GGCACCCAGA GTACAACAGA CTCTTGCTCG CTAACGACCT CATGCTCATC      240
AAGTTGGACG AATCCGTGTC CGAGTCTGAC ACCATCCGGA GCATCAGCAT TGCTTCGCAG      300
TGCCCTACCG CGGGGAACCT TGCCTCGTN TCTGGCTGGG GTCTGCTGGC GAACGGCAGA      360
ATGCCTACCG TGCTGCACTG CGTGAACGTG TCGGTGGTGT CTGAGGANGT CTGCAGTAAG      420
CTCTATGACC CGCTGTACCA CCCAGCATG TTCTGCGCCG GCGGAGGGCA AGACCAGAAG      480
GACTCCTGCA ACGGTGACTC TGGGGGGCCC CTGATCTGCA ACGGGTACTT GCAGGGCCTT      540
GTGTCTTTTC GAAAAGCCCC GTGTGGCCAA CTTGGCGTGC CAGGTGTCTA CACCAACCTC      600
TGCAAATTCA CTGAGTGGAT AGAGAAAACC GTCCAGNCCA GTTAACTCTG GGGACTGGGA      660
ACCCATGAAA TTGACCCCCA AATACATCCT GCGGAANGAA TTCAGGAATA TCTGTTCCCA      720
GCCCCCTCCT CCTCAGGCCC AGGAGTCCAG GCCCCCAGCC CCTCCTCCCT CAAACCAAGG      780
GTACAGATCC CCAGCCCCCTC CTCCTCAGA CCCAGGAGTC CAGACCCCCC AGCCCCCTNT      840
CCNTCAGACC CAGGAGTCCA GCCCTCCTC CNTCAGACGC AGGAGTCCAG ACCCCCCAGC      900
CCNTCNTCCG TCAGACCCAG GGGTGCAGGC CCCCCACCCC TCNTCCNTCA GAGTCAGAGG      960
TCCAAGCCCC CAACCCCTCG TTCCCCAGAC CCAGAGGTNC AGGTCCCAGC CCCTCCTCCC     1020
TCAGACCCAG CGGTCCAATG CCACCTAGAN TNTCCCTGTA CACAGTGCCC CCTTGTGGCA     1080
NGTTGACCCA ACCTTACCAG TTGGTTTTTC ATTTTTTGTC CCTTTCCCTT AGATCCAGAA     1140
ATAAAGTNTA AGAGAAGCGC AAAAAAA                      1167
  
```

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

```

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1              5              10              15

Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
      20              25              30

Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
      35              40              45

Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu
      50              55              60
  
```

Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
65 70 75 80

Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
85 90 95

Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met
100 105 110

Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val
115 120 125

Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala
130 135 140

Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly
145 150 155 160

Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys
165 170 175

Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys
180 185 190

Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser
195 200 205

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GCGCACTCGC	AGCCCTGGCA	GGCGGCACTG	GTCATGGAAA	ACGAATTGTT	CTGCTCGGGC	60
GTCCTGGTGC	ATCCGCAGTG	GGTGCTGTCA	GCCGCACACT	GTTTCCAGAA	CTCCTACACC	120
ATCGGGCTGG	GCCTGCACAG	TCTTGAGGCC	GACCAAGAGC	CAGGGAGCCA	GATGGTGGAG	180
GCCAGCCTCT	CCGTACGGCA	CCCAGAGTAC	AACAGACCCT	TGCTCGCTAA	CGACCTCATG	240
CTCATCAAGT	TGGACGAATC	CGTGTCCGAG	TCTGACACCA	TCCGGAGCAT	CAGCATTGCT	300
TCCGAGTGCC	CTACCGCGGG	GAACCTCTGC	CTCGTTTCTG	GCTGGGGTCT	GCTGGCGAAC	360
GATGCTGTGA	TTGCCATCCA	GTCCCAGACT	GTGGGAGGCT	GGGAGTGTGA	GAAGCTTTCC	420
CAACCCTGGC	AGGGTTGTAC	CATTTCGGCA	ACTTCCAGTG	CAAGGACGTC	CTGCTGCATC	480
CTCACTGGGT	GCTCACTACT	GCTCACTGCA	TCACCCGGAA	CACTGTGATC	AAC TAGCCAG	540
CACCATAGTT	CTCCGAAGTC	AGACTATCAT	GATTACTGTG	TTGACTGTGC	TGTCTATTGT	600
ACTAACCATG	CCGATGTTTA	GGTGAAATTA	GCGTCACTTG	GCCTCAACCA	TCTTGGTATC	660
CAGTTATCCT	CACTGAATTG	AGATTTCCTG	CTTCAGTGTC	AGCCATTCCC	ACATAATTTT	720
TGACCTACAG	AGGTGAGGGA	TCATATAGCT	CTTCAAGGAT	GCTGGTACTC	CCCTCACAAA	780
TTCATTTTCT	CTGTTGTAGT	GAAAGGTGCG	CCCTCTGGAG	CCTCCAGGG	TGGGTGTGCA	840
GGTCACAATG	ATGAATGTAT	GATCGTGTTC	CCATTACCCA	AAGCCTTTAA	ATCCCTCATG	900
CTCAGTACAC	CAGGGCAGGT	CTAGCATTTT	TTCATTTAGT	GTATGCTGTC	CATTCATGCA	960
ACCACCTCAG	GACTCCTGGA	TTCTCTGCCT	AGTTGAGCTC	CTGCATGCTG	CCTCCTTGGG	1020
GAGGTGAGGG	AGAGGGCCCA	TGTTTCAATG	GGATCTGTGC	AGTTGTAACA	CATTAGGTGC	1080

TTAATAAACA GAAGCTGTGA TGTAAAAA AAAAAA

1119

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1             5             10             15

Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
      20             25             30

Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
      35             40             45

Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu
      50             55             60

Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
      65             70             75             80

Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
      85             90             95

Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val
      100            105            110

Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu
      115            120            125

Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg
      130            135            140

Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser
      145            150            155            160

Pro Gly Thr Leu

```

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTGGAGTGCC TTGGTGTTC AAGCCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT

60

110

CCAGCTGCCC	CCGGCCGGGG	GATGCGAGGC	TCGGAGCACC	CTTGCCCGGC	TGTGATTGCT	120
GCCAGGCACT	GTTTCATCTCA	GCTTTTCTGT	CCCTTTGCTC	CCGGCAAGCG	CTTCTGCTGA	180
AAGTTCATAT	CTGGAGCCTG	ATGTCTTAAC	GAATAAAGGT	CCCATGCTCC	ACCCGAAAAA	240
AAAAAAAAAA						250

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ACTAGTCCAG	TGTGGTGGA	TTCCATTGTG	TTGGGCCCAA	CACAATGGCT	ACCTTTAACA	60
TCACCCAGAC	CCCGCCCTG	CCCGTGCCCC	ACGCTGCTGC	TAACGACAGT	ATGATGCTTA	120
CTCTGCTACT	CGGAACTAT	TTTTATGTAA	TTAATGTATG	CTTTCTTGTT	TATAAATGCC	180
TGATTTAAAA	AAAAAAAAAA	AA				202

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCCYTTTGKT	NAGGTTTKKG	AGACAMCCCK	AGACCTWAAN	CTGTGTCACA	GACTTCYNNG	60
AATGTTTAGG	CAGTGCTAGT	AATTCYTCG	TAATGATTCT	GTTATTACTT	TCCTNATTCT	120
TTATTCCTCT	TTCTCTGAA	GATTAATGAA	GTTGAAAATT	GAGGTGGATA	AATACAAAAA	180
GGTAGTGTGA	TAGTATAAGT	ATCTAAGTGC	AGATGAAAGT	GTGTTATATA	TATCCATTCA	240
AAATTATGCA	AGTTAGTAAT	TACTCAGGGT	TAACATAAAT	ACTTTAATAT	GCTGTTGAAC	300
CTACTCTGTT	CCTTGGCTAG	AAAAAATTAT	AAACAGGACT	TTGTTAGTTT	GGGAAGCCAA	360
ATTGATAATA	TTCTATGTTT	TAAAAGTTGG	GCTATACATA	AATTATTAAG	AAATATGGAW	420
TTTTATTCCC	AGGAATATGG	KGTTTCATTTT	ATGAATATTA	CSCRGGATAG	AWGTWTGAGT	480
AAAAYCAGTT	TTGGTWAATA	YGTWAATATG	TCMTAAATAA	ACAAKGCTTT	GACTTATTTT	540
CAAAAAAAA	AAAAAAA					558

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

ACAGGGWTTK	GRGGATGCTA	AGSCCCCRGA	RWTYGTTTGA	TCCAACCCTG	GCTTWTTTTC	60
AGAGGGGAAA	ATGGGGCCTA	GAAGTTACAG	MSCATYTAGY	TGGTGCGMTG	GCACCCCTGG	120
CSTCACACAG	ASTCCCGAGT	AGCTGGGACT	ACAGGCACAC	AGTCACTGAA	GCAGGCCCTG	180
TTWGCAATTC	ACGTTGCCAC	CTCCAACCTA	AACATTCTTC	ATATGTGATG	TCCTTAGTCA	240
CTAAGGTTAA	ACTTTCCAC	CCAGAAAAGG	CAACTTAGAT	AAAATCTTAG	AGTACTTTCA	300
TACTMTTCTA	AGTCCTCTTC	CAGCCTCACT	KKGAGTCCTM	CYTGGGGGTT	GATAGGAANT	360
NTCTCTTGGC	TTTCTCAATA	AARTCTCTAT	YCATCTCATG	TTTAATTG	TACGCATARA	420

AWTGSTGARA AAATTAAAAT GTTCTGGTTY MACTTTAAAA ARAAAAAAAAA AAAAAAAAAA 479

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

AGGCGGGAGC	AGAAGCTAAA	GCCAAAGCCC	AAGAAGAGTG	GCAGTGCCAG	CACTGGTGCC	60
AGTACCACTA	CCAATAACAG	TGCCAGTGCC	AGTGCCAGCA	CCAGTGGTGG	CTTCAGTGCT	120
GGTGCCAGCC	TGACCGCCAC	TCTCACATTT	GGGCTCTTCG	CTGGCCTTGG	TGGAGCTGGT	180
GCCAGCACCA	GTGGCAGCTC	TGGTGCCTGT	GGTTTCTCCT	ACAAGTGAGA	TTTtagatat	240
TGTTAATCCT	GCCAGTCTTT	CTCTTCAAGC	CAGGGTGCAT	CCTCAGAAAC	CTACTCAACA	300
CAGCACTCTA	GGCAGCCACT	ATCAATCAAT	TGAAGTTGAC	ACTCTGCATT	ARATCTATTT	360
GCCATTTCAA	AAAAAAAAAA	AAAA				384

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ACCGAATTGG	GACCGCTGGC	TTATAAGCGA	TCATGTYINT	CCRGATKAC	CTCAACGAGC	60
AGGGAGATCG	AGTCTATACG	CTGAAGAAAT	TTGACCCGAT	GGGACAACAG	ACCTGCTCAG	120
CCCATCCTGC	TCGGTTCTCC	CCAGATGACA	AATACTCTSG	ACACCGAATC	ACCATCAAGA	180
AACGCTTCAA	GGTGCTCATG	ACCCAGCAAC	CGCGCCCTGT	CCTCTGAGGG	TCCCTTAAAC	240
TGATGTCTTT	TCTGCCACCT	GTTACCCCTC	GGAGACTCCG	TAACCAAAC	CTTCGGACTG	300
TGAGCCCTGA	TGCCTTTTTC	CCAGCCATAC	TCTTTGGCAT	CCAGTCTCTC	GTGGCGATTG	360
ATTATGCTTG	TGTGAGGCAA	TCATGGTGGC	ATCACCCATA	AAGGGAACAC	ATTTGACTTT	420
TTTTTCTCAT	ATTTTAAATT	ACTACMAGAW	TATTWMAGAW	WAAATGAWTT	GAAAACTST	480
TAAAAAAAAA	AAAAAA					496

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GCTGGTAGCC	TATGGCGKGG	CCCACGGAGG	GGCTCCTGAG	GCCACGGRAC	AGTGAATTCC	60
CAAGTATCYT	GCGCSGCGTC	TTCTACCGTC	CCTACCTGCA	GATCTTCGGG	CAGATTCCCC	120
AGGAGGACAT	GGACGTGGCC	CTCATGGAGC	ACAGCAACTG	YTCGTGGGAG	CCCGGCTTCT	180
GGGCACACCC	TCCTGGGGCC	CAGGCGGGCA	CCTGCGTCTC	CCAGTATGCC	AACTGGCTGG	240
TGGTGCTGCT	CCTCGTCATC	TTCTGCTCG	TGGCCAACAT	CCTGCTGGTC	AACTTGCTCA	300
TTGCCATGTT	CAGTTACACA	TTGGGCAAAG	TACAGGGCAA	CAGCGATCTC	TACTGGGAAG	360
GCGCAGCGTT	ACCGCCTCAT	CCGG				384

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

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GAGTTAGCTC CTCCACAACC TTGATGAGGT CGTCTGCAGT GGCCTCTCGC TTCATACCGC      60
TNCCATCGTC ATACTGTAGG TTTGCCACCA CYTCCTGGCA TCTTGGGGCG GCNTAATATT      120
CCAGGAAACT CTCAATCAAG TCACCGTCGA TGAAACCTGT GGGCTGGTTC TGTCTTCCGC      180
TCGGTGTGAA AGGATCTCCC AGAAGGAGTG CTCGATCTTC CCCACACTTT TGATGACTTT      240
ATTGAGTCGA TTCTGCATGT CCAGCAGGAG GTTGTACCAG CTCTCTGACA GTGAGGTCAC      300
CAGCCCTATC ATGCCGTTGA MCGTGCCGAA GARCACCGAG CCTTGTGTGG GGGKKGAAGT      360
CTCACCCAGA TTCTGCATTA CCAGAGAGCC GTGGCAAAAG ACATTGACAA ACTCGCCCAG      420
GTGGA AAAAG AMCAMCTCCT GGARGTGCTN GCCGCTCCTC GTCMGTGGT GGCAGCGCTW      480
TCCTTTTGAC ACACAAACAA GTTAAAGGCA TTTTCAGCCC CCAGAAANTT GTCATCATCC      540
AAGATNTCGC ACAGCACTNA TCCAGTTGGG ATTAAAT                                577

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(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

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AACATCTTCC TGTATAATGC TGTGTAATAT CGATCCGATN TTGTCTGSTG AGAATYCATW      60
ACTKGGAAAA GMAACATTAA AGCCTGGACA CTGGTATTAA AATTCACAAT ATGCAACACT      120
TTAAACAGTG TGTCAATCTG CTCCCYNAC TTTGTCATCA CCAGTCTGGG AAKAAGGGTA      180
TGCCCTATTG ACACCTGTTA AAAGGGCGCT AAGCATTTTT GATTCAACAT CTTTTTTTTT      240
GACACAAGTC CGAAAAAAGC AAAAGTAAAC AGTTATYAAT TTGTTAGCCA ATTCACTTTC      300
TTCATGGGAC AGAGCCATYT GATTTAAAAA GCAAATTGCA TAATATTGAG CTTYGGGAGC      360
TGATATTTGA GCGGAAGAGT AGCCTTTCTA CTTACCAGA CAAACTCCC TTTCATATTG      420
GGATGTTNAC NAAAGTWATG TCTCTWACAG ATGGGATGCT TTTGTGGCAA TTCTGTTCTG      480
AGGATCTCCC AGTTTATTTA CCACTTGCAC AAGAAGGCGT TTTCTTCCTC AGGC                                534

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(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 761 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

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AGAAACCACT ATCTCTNAAA ACAACCTCTC ATACCTTGTG GACCTAATTT TGTGTGCGTG      60
TGTGTGTGCG CGCATATTAT ATAGACAGGC ACATCTTTTT TACTTTTGTA AAAGCTTATG      120
CCTCTTTGGT ATCTATATCT GTGAAAGTTT TAATGATCTG CCATAATGTC TTGGGGACCT      180
TTGTCTTCTG TGTAATGGT ACTAGAGAAA ACACCTATNT TATGAGTCAA TCTAGTTNGT      240
TTTATTCGAC ATGAAGGAAA TTTCCAGATN ACAACACTNA CAAACTCTCC CTKGACKARG      300
GGGGACAAAG AAAAGCAAAA CTGAMCATAA RAAACAATWA CCTGGTGAGA ARTTGCATAA      360
ACAGAAATWR GGTAGTATAT TGAARNACAG CATCATTAAA RMGTTWTKTT WTTCTCCCTT      420

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GCAAAAAACA	TGTACNGACT	TCCCGTTGAG	TAATGCCAAG	TTGTTTTTTT	TATNATAAAA	480
CTTGCCCTTC	ATTACATGTT	TNAAAGTGGT	GTGGTGGGCC	AAAATATTGA	AATGATGGAA	540
CTGACTGATA	AAGCTGTACA	AATAAGCAGT	GTGCCTAACA	AGCAACACAG	TAATGTTGAC	600
ATGCTTAATT	CACAAATGCT	AATTTTATTA	TAAATGTTTG	CTAAAATACA	CTTTGAACTA	660
TTTTTCTGTN	TTCCCGAGAGC	TGAGATNTTA	GATTTTATGT	AGTATNAAGT	GAAAAANTAC	720
GAAAAATAATA	ACATTGAAGA	AAAANANAAA	AAANAAAAAA	A		761

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TTTTTTTTTT	TTTGCCGATN	CTACTATTTT	ATTGCAGGAN	GTGGGGGTGT	ATGCACCGCA	60
CACCGGGGCT	ATNAGAAGCA	AGAAGGAAGG	AGGGAGGGCA	CAGCCCCTTG	CTGAGCAACA	120
AAGCCGCTTG	CTGCCTTCTC	TGTCTGTCTC	CTGGTGCAGG	CACATGGGGA	GACCTTCCCC	180
AAGGCAGGGG	CCACCAGTCC	AGGGGTGGGA	ATACAGGGGG	TGGGANGTGT	GCATAAGAAG	240
TGATAGGCAC	AGGCCACCCG	GTACAGACCC	CTCGGCTCCT	GACAGGTNGA	TTTCGACCAG	300
GTCATTGTGC	CCTGCCCAGG	CACAGCGTAN	ATCTGGAAAA	GACAGAATGC	TTTCCTTTTC	360
AAATTTGGCT	NGTCATNGAA	NGGGCANTTT	TCCAANTTNG	GCTNGGTCTT	GGTACNCTTG	420
GTTCGGCCCA	GCTCCNCGTC	CAAAAANTAT	TCACCCNNCT	CCNAATTGCT	TGCNGGNCCC	480
CC						482

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TTTTTTTTTT	TTTTAAACA	GTTTTTCACA	ACAAAATTTA	TTAGAAGAAT	AGTGGTTTTG	60
AAAACCTCTCG	CATCCAGTGA	GAACCTACCAT	ACACCACATT	ACAGCTNGGA	ATGTNCTCCA	120
AATGTCTGGT	CAAATGATAC	AATGGAACCA	TTCAATCTTA	CACATGCACG	AAAGAACAAG	180
CGCTTTTGAC	ATACAATGCA	CAAAAAAAAA	AGGGGGGGGG	GACCACATGG	ATTAAAATTT	240
TAAGTACTCA	TCACATACAT	TAAGACACAG	TTCTAGTCCA	GTGNAAAATC	AGAACTGCNT	300
TGAAAAATTT	CATGTATGCA	ATCCAACCAA	AGAACTTNAT	TGGTGATCAT	GANTNCTCTA	360
CTACATCNAC	CTTGATCATT	GCCAGGAACN	AAAAGTTNAA	ANCACNCNGT	ACAAAAANAA	420
TCTGTAATTN	ANTTCAACCT	CCGTACNGAA	AAATNTTNT	TATACACTCC	C	471

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAGGGATTGA	AGGTCTGTTC	TASTGTCGGM	CTGTTCAGCC	ACCAACTCTA	ACAAGTTGCT	60
GTCTTCCACT	CACTGTCTGT	AAGCTTTTTA	ACCCAGACWG	TATCTTCATA	AATAGAACAA	120

ATTCTTCACC	AGTCACATCT	TCTAGGACCT	TTTTGGATTC	AGTTAGTATA	AGCTCTTCCA	180
CTTCCTTTGT	TAAGACTTCA	TCTGGTAAAG	TCTTAAGTTT	TGTAGAAAGG	AATTYAATTG	240
CTCGTTCTCT	AACAATGTCC	TCTCCTTGAA	GTATTTGGCT	GAACAACCCA	CCTAAAGTCC	300
CTTTGTGCAT	CCATTTTAAA	TATACTTAAT	AGGGCATTGK	TNCACTAGGT	TAAATTCTGC	360
AAGAGTCATC	TGTCTGCAAA	AGTTGCGTTA	GTATATCTGC	CA		402

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAGCTCGGAT	CCAATAATCT	TTGTCTGAGG	GCAGCACACA	TATNCAGTGC	CATGGNAACT	60
GGTCTACCCC	ACATGGGAGC	AGCATGCCGT	AGNTATATAA	GGTCATTCCC	TGAGTCAGAC	120
ATGCYTYTTT	GAYTACCGTG	TGCCAAGTGC	TGGTGATTCT	YAACACACYT	CCATCCCGYT	180
CTTTTGTGGA	AAAAGTGGCA	CTTKTCTGGA	ACTAGCARGA	CATCACTTAC	AAATTCACCC	240
ACGAGACACT	TGAAAGGTGT	AACAAAGCGA	YTCTTGCAAT	GCTTTTGTGC	CCTCCGGCAC	300
CAGTTGTCAA	TACTAACCCG	CTGGTTTGCC	TCCATCACAT	TTGTGATCTG	TAGCTCTGGA	360
TACATCTCCT	GACAGTACTG	AAGAACTTCT	TCTTTTGTTC	CAAAAGCARG	TCTTGGTGCC	420
TGTTGGATCA	GGTTCCCAT	TCCCAGTCYG	AATGTTTACA	TGGCATATTT	WACTTCCAC	480
AAAACATTGC	GATTTGAGGC	TCAGCAACAG	CAAATCCTGT	TCCGGCATTG	GCTGCAAGAG	540
CCTCGATGTA	GCCGCGCCAGC	GCCAAGGCAG	GCGCCGTGAG	CCCCACCAGC	AGCAGAAGCA	600
G						601

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

ATACAGCCCA	NATCCCACCA	CGAAGATGCG	CTTGTTGACT	GAGAACCTGA	TGCGGTCACT	60
GGTCCCCTG	TAGCCCCAGC	GACTCTCCAC	CTGCTGGAAG	CGGTTGATGC	TGCACTCYTT	120
CCCAACGCAG	GCAGMAGCGG	GSCCGGTCAA	TGAAGTCCAY	TCGTGGCTTG	GGGTKGACGG	180
TKAAGTGACG	GAAGAGGCTG	ACCACCTCGC	GGTCCACCAG	GATGCCCCGAC	TGTGCGGGAC	240
CTGCAGCGAA	ACTCCTCGAT	GGTCATGAGC	GGGAAGCGAA	TGAGGCCAG	GGCCTTGCCC	300
AGAACCTTCC	GCCTGTTCTC	TGGCGTCACC	TGCAGCTGCT	GCCGCTGACA	CTCGGCCTCG	360
GACCAGCGGA	CAAACGGCRT	TGAACAGCCG	CACCTCACGG	ATGCCAGTG	TGTGCGGCTC	420
CAGGAMMGS	ACCAGCGTGT	CCAGGTCAAT	GTCGGTGAAG	CCCTCCGCGG	GTRATGGCGT	480
CTGCAGTGTT	TTGTGCGATG	TTCTCCAGGC	ACAGGCTGGC	CAGCTGCGGT	TCATCGAAGA	540
GTCGCGCCTG	CGTGAGCAGC	ATGAAGGCGT	TGTGCGCTCG	CAGTTCTTCT	TCAGGAAGTC	600
CACGCAAT						608

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAACGGCTGG	ACCTTGCCCTC	GCATTGTGCT	TGCTGGCAGG	GAATACCTTG	GCAAGCAGYT	60
CCAGTCCGAG	CAGCCCCAGA	CCGCTGCCGC	CCGAAGCTAA	GCCTGCCTCT	GGCCTTCCCC	120
TCCGCCTCAA	TGCAGAACCA	GTAAGTGGGAG	CACTGTGTTT	AGAGTTAAGA	GTGAACACTG	180
TTTGATTTTA	CTTGGGAATT	TCCTCTGTTA	TATAGCTTTT	CCCAATGCTA	ATTTCCAAAC	240
AACAACAACA	AAATAACATG	TTTGCCTGTT	AAGTTGTATA	AAAGTAGGTG	ATTCTGTATT	300
TAAAGAAAAT	ATTACTGTTA	CATATACTGC	TTGCAATTTT	TGTATTTATT	GKTNCTSTGG	360
AAATAAATAT	AGTTATTAAA	GGTTGTCANT	CC			392

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CCSTTKGAGG	GGTKAGGKYC	CAGTTYCCGA	GTGGAAGAAA	CAGGCCAGGA	GAAGTGCCTG	60
CCGAGCTGAG	GCAGATGTTT	CCACAGTGAC	CCCCAGAGCC	STGGGSTAT	GTCTCTGACC	120
CCTCNCAAGG	AAAGACCACS	TTCTGGGGAC	ATGGGCTGGA	GGGCAGGACC	TAGAGGCACC	180
AAGGGAAGGC	CCCATTCGGG	GGSTGTTCCT	CGAGGAGGAA	GGGAAGGGGC	TCTGTGTGCC	240
CCCCASGAGG	AAGAGGCCCT	GAGTCCTGGG	ATCAGACACC	CCTTCACGTG	TATCCCCACA	300
CAAATGCAAG	CTCACCAAGG	TCCCCTCTCA	GTCCCCTTCC	STACACCCTG	AMCGGCCACT	360
GSCSCACACC	CACCCAGAGC	ACGCCACCCG	CCATGGGGAR	TGTGCTCAAG	GARTCGCNGG	420
GCARCGTGGA	CATCTNGTCC	CAGAAGGGGG	CAGAATCTCC	AATAGANGGA	CTGARCMSTT	480
GCTNANAAAA	AAAAANAAAA	AA				502

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GGTTACTTGG	TTTCATTGCC	ACCACTTAGT	GGATGTCATT	TAGAACCATT	TTGTCTGCTC	60
CCTCTGGAAG	CCTTGCGCAG	AGCGGACTTT	GTAATTGTTG	GAGAATAACT	GCTGAATTTT	120
WAGCTGTTTK	GAGTTGATTS	GCACCACTGC	ACCCACAAC	TCAATATGAA	AACYAWTTGA	180
ACTWATTTAT	TATCTTGTGA	AAAGTATAAC	AATGAAAATT	TTGTTCATAC	TGTATTKATC	240
AAGTATGATG	AAAAGCAAWA	GATATATATT	CTTTTATTAT	GTTAAATTAT	GATTGCCATT	300
ATTAATCGGC	AAAATGTGGA	GTGTATGTTT	TTTTCACAGT	AATATATGCC	TTTTGTAACT	360
TCACTTGGTT	ATTTTATTGT	AAATGARTTA	CAAAATTCTT	AATTTAAGAR	AATGGTATGT	420
WATATTTATT	TCATTAATTT	CTTTCCTKGT	TTACGTWAAT	TTTGAAAAAG	WTGCATGATT	480
TCTTGACAGA	AATCGATCTT	GATGCTGTGG	AAGTAGTTTG	ACCCACATCC	CTATGAGTTT	540
TTCTTAGAAT	GTATAAAGGT	TGTAGCCCAT	CNAACTTCAA	AGAAAAAAT	GACCACATAC	600
TTTGCAATCA	GGCTGAAATG	TGGCATGCTN	TTCTAATTCC	AACTTTATAA	ACTAGCAAAN	660
AAGTG						665

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

TTTNTTTTTT	TTTTTTTTGC	AGGAAGGATT	CCATTATTGG	TGGATGCATT	TTCACAATAT	60
ATGTTTATTG	GAGCGATCCA	TTATCAGTGA	AAAGTATCAA	GTGTTTATAA	NATTTTTAGG	120
AAGGCAGATT	CACAGAACAT	GCTNGTCNGC	TTGCAGTTTT	ACCTCGTANA	GATNACAGAG	180
AATTATAGTC	NAACCAGTAA	ACNAGGAATT	TACTTTTCAA	AAGATTAAAT	CCAAACTGAA	240
CAAAATTCTA	CCCTGAAACT	TACTCCATCC	AAATATTGGA	ATAANAGTCA	GCAGTGATAC	300
ATTCTCTTCT	GAACTTTAGA	TTTTCTAGAA	AAATATGTAA	TAGTGATCAG	GAAGAGCTCT	360
TGTTCAAAAG	TACAACNAAG	CAATGTTCCC	TTACCATAGG	CCTTAATTCA	AACTTTGATC	420
CATTTCACTC	CCATCACGGG	AGTCAATGCT	ACCTGGGACA	CTTGTATTTT	GTTTCATNCTG	480
ANCNTGGCTT	AA					492

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

TTNTTTTTGN	ATTTCACTCT	GTANNAANTA	TTTTATTAT	GTTTATTANA	AAAATATNAA	60
TGTNTCCACN	ACAAATCATN	TTACNTNAGT	AAGAGGCCAN	CTACATTGTA	CAACATACAC	120
TGAGTATATT	TTGAAAAGGA	CAAGTTTAAA	GTANACNCAT	ATTGCCGANC	ATANCACATT	180
TATACATGGC	TTGATTGATA	TTAGCACAG	CANAACTGA	GTGAGTTACC	AGAAANAAAT	240
NATATATGTC	AATCNGATTT	AAGATACAAA	ACAGATCCTA	TGGTACATAN	CATCNTGTAG	300
GAGTTGTGGC	TTTATGTTTA	CTGAAAGTCA	ATGCAGTTCC	TGTACAAAGA	GATGGCCGTA	360
AGCATTCTAG	TACCTCTACT	CCATGGTTAA	GAATCGTACA	CTTATGTTTA	CATATGTNCA	420
GGGTAAGAAT	TGTGTTAAGT	NAANTTATGG	AGAGGTCCAN	GAGAAAAATT	TGATNCAA	478

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

AGTGACTTGT	CCTCCAACAA	AACCCCTTGA	TCAAGTTTGT	GGCACTGACA	ATCAGACCTA	60
TGCTAGTTCC	TGTCATCTAT	TCGCTACTAA	ATGCAGACTG	GAGGGGACCA	AAAAGGGGCA	120
TCAACTCCAG	CTGGATTATT	TTGGAGCCTG	CAAATCTATT	CCTACTTGTA	CGGACTTTGA	180
AGTGATTTCAG	TTTCCTCTAC	GGATGAGAGA	CTGGCTCAAG	AATATCCTCA	TGCAGCTTTA	240
TGAAGCCNAC	TCTGAACACG	CTGTTTATCT	NAGATGAGAA	NCAGAGAAAT	AAAGTCNAGA	300
AAATTTACCT	GGANGAAAAG	AGGCTTTNGG	CTGGGGACCA	TCCCATTGAA	CCTTCTCTTA	360
ANGGACTTTA	AGAANAAACT	ACCACATGTN	TGTNGTATCC	TGGTGCCNGG	CCGTTTANTG	420
AACNTNGACN	NCACCCTTNT	GGAATANANT	CTTGACNGCN	TCCTGAACCT	GCTCCTCTGC	480
GA						482

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CGGCCGCAAG	TGCAACTCCA	GCTGGGGCCG	TGCGGACGAA	GATTCTGCCA	GCAGTTGGTC	60
CGACTGCGAC	GACGGCGGCG	GCGACAGTCG	CAGGTGCAGC	GCGGGCGCCT	GGGGTCTTGC	120
AAGGCTGAGC	TGACGCCGCA	GAGGTCGTGT	CACGTCCCAC	GACCTTGACG	CCGTCGGGGA	180
CAGCCGGAAC	AGAGCCCGGT	GAANGCGGGA	GGCCTCGGGG	AGCCCCCTCG	GAAGGGCGGG	240
CCGAGAGATA	CGCAGGTGCA	GGTGCCGCC				270

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

TTTTTTTTTT	TTTTGGAATC	TACTGCGAGC	ACAGCAGGTC	AGCAACAAGT	TTATTTTGCA	60
GCTAGCAAGG	TAACAGGGTA	GGGCATGGTT	ACATGTTCAG	GTCAACTTCC	TTTGTCGTGG	120
TTGATTGGTT	TGTCTTTATG	GGGGCGGGGT	GGGGTAGGGG	AAANCGAAGC	ANAANTAACA	180
TGGAGTGGGT	GCACCTTCCC	TGTAGAACCT	GGTTACNAAA	GCTTGGGGCA	GTTCACTTGG	240
TCTGTGACCG	TCATTTTCTT	GACATCAATG	TTATTAGAAG	TCAGGATATC	TTTTAGAGAG	300
TCCACTGTNT	CTGGAGGGAG	ATTAGGGTTT	CTTGCCAANA	TCCAANCAAA	ATCCACNTGA	360
AAAAGTTGGA	TGATNCANGT	ACNGAATACC	GANGGCATAN	TTCTCATANT	CGGTGGCCA	419

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TTTNTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
TGGCACTTAA	TCCATTTTTA	TTTCAAAATG	TCTACAAANT	TTNAATNCNC	CATTATACNG	120
GTNATTTTNC	AAAATCTAAA	NNTTATTCAA	ATNTNAGCCA	AANTCCTTAC	NCAAATNNAA	180
TACNCNCAAA	AATCAAAAAT	ATACNTNTCT	TTCAGCAAAAC	TTNGTTACAT	AAATTA AAAA	240
AATATATACG	GCTGGTGT TT	TCAAAGTACA	ATTATCTTAA	CACTGCAAAC	ATNTTTNNAA	300
GGAAC TAAAA	TAAAAA AAAA	CACTNCCGCA	AAGGT TAAAG	GGAACAACAA	ATT CNTTTTA	360
CAACANCNNC	NATTATAAAA	ATCATATCTC	AAATCTTAGG	GGAATATATA	CTTCACACNG	420
GGATCTTAAC	TTT TACTNCA	CTTTGTTTAT	TTTTTTTANAA	CCATTGTNTT	GGGCCCCACA	480
CAATGGNAAT	NCCNCCNCNC	TGGACTAGT				509

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TTTTTTTTTT	TTTTTTTTGA	CCCCCTCTT	ATAAAAACA	AGTTACCATT	TTATTTTACT	60
TACACATATT	TATTTTATAA	TTGGTATTAG	ATATTCAAAA	GGCAGCTTTT	AAAATCAAAC	120
TAAATGGAAA	CTGCCTTAGA	TACATAATTC	TTAGGAATTA	GCTTAAAAATC	TGCCTAAAGT	180
GAAAATCTTC	TCTAGCTCTT	TTGACTGTAA	ATTTTGTGACT	CTTGTA AAC	ATCCAAATTC	240
ATTTTCTTGG	TCTTAAAAAT	TATCTAATCT	TTCCATTTTT	TCCCTATTCC	AAGTCAATTT	300
GCTTCTCTAG	CCTCATTTCC	TAGCTCTTAT	CTACTATTAG	TAAGTGGCTT	TTTCCTAAA	360
AGGGAACA	GGAAGAGANA	ATGGCACACA	AAACAAACAT	TTTATATTCA	TATTTCTACC	420
TACGTTAATA	AAATAGCATT	TTGTGAAGCC	AGCTCAAAAG	AAGGCTTAGA	TCCTTTTATG	480
TCCATTTTAG	TCACTAAACG	ATATCNAAAG	TGCCAGAATG	CAAAGGTTT	GTGAACATTT	540
ATTCAAAAGC	TAATATAAGA	TATTTACAT	ACTCATCTTT	CTG		583

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TTTTTTTTNT	TTTTTTTTTT	TTTTTNTCTC	TTCTTTTTTT	TTGANAATGA	GGATCGAGTT	60
TTTCACTCTC	TAGATAGGGC	ATGAAGAAAA	CTCATCTTTC	CAGCTTTAAA	ATAACAATCA	120
AATCTCTTAT	GCTATATCAT	ATTTTAAGTT	AACTAATGA	GTCAGTGGCT	TATCTTCTCC	180
TGAAGGAAAT	CTGTTCATT	TTCTCATTCA	TATAGTTATA	TCAAGTACTA	CCTTGATAT	240
TGAGAGGTTT	TTCTTCTCTA	TTTACACATA	TATTTCCATG	TGAATTGTGA	TCAAACCTTT	300
ATTTTCATGC	AAACTAGAAA	ATAATGTNTT	CTTTTGCCATA	AGAGAAGAGA	ACAATATNAG	360
CATTACAAAA	CTGCTCAAAT	TGTTTGTTAA	GNTTATCCAT	TATAATTAGT	TNGGCAGGAG	420
CTAATACAAA	TCACATTTAC	NGACNAGCAA	TAATAAACT	GAAGTACCAG	TTAAATATCC	480
AAAATAATTA	AAGGAACATT	TTAGCCTGG	GTATAATTAG	CTAATTCAT	TTACAAGCAT	540
TTATTNAGAA	TGAATTCACA	TGTTATTATT	CNTAGCCCA	ACACAATGG		589

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

TTTTNTTTTT	TTTTTTCAGT	AATAATCAGA	ACAATATTTA	TTTTTATATT	TAAAATTCAT	60
AGAAAAGTGC	CTTACATTTA	ATAAAAGTTT	GTTTCTCAAA	GTGATCAGAG	GAATTAGATA	120
TNGTCTTGAA	CACCAATATT	AATTTGAGGA	AAATACACCA	AAATACATTA	AGTAAATTAT	180
TTAAGATCAT	AGAGCTTGTA	AGTGAAAAGA	TAAAATTTGA	CCTCAGAAAC	TCTGAGCATT	240
AAAAATCCAC	TATTAGCAAA	TAAATTACTA	TGGACTTCTT	GCTTTAATTT	TGTGATGAAT	300
ATGGGGTGTC	ACTGGTAAAC	CAACACATTC	TGAAGGATAC	ATTACTTAGT	GATAGATTCT	360
TATGTACTTT	GCTANATNAC	GTGGATATGA	GTTGACAAGT	TTCTCTTTCT	TCAATCTTTT	420
AAGGGGCNGA	NGAAATGAGG	AAGAAAAGAA	AAGGATTACG	CATACTGTTC	TTTCTATNGG	480
AAGGATTAGA	TATGTTTCCT	TTGCCAATAT	TAAAAAATA	ATAATGTTTA	CTACTAGTGA	540
AACCC						545

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TTTTTTTTTT	TTTTTAGTC	AAGTTTCTNA	TTTTTATTAT	AATTAAAGTC	TTGGTCATTT	60
CATTIATTAG	CTCTGCAACT	TACATATTTA	AATTAAAGAA	ACGTTNNTAG	ACAACTGTNA	120
CAATTTATAA	ATGTAAGGTG	CCATTATTGA	GTANATATAT	TCCTCCAAGA	GTGGATGTGT	180
CCCTTCTCCC	ACCAACTAAT	GAANCAGCAA	CATTAGTTTA	ATTTTATTAG	TAGATNATAC	240
ACTGCTGCAA	ACGCTAATTC	TCTTCTCCAT	CCCCATGTNG	ATATTGTGTA	TATGTGTGAG	300
TTGGTNAGAA	TGCATCANCA	ATCTNACAAT	CAACAGCAAG	ATGAAGCTAG	GCNTGGGCTT	360
TCGGTGAAAA	TAGACTGTGT	CTGTCTGAAT	CAAATGATCT	GACCTATCCT	CGGTGGCAAG	420
AACTCTTCGA	ACCGCTTCCT	CAAAGGCNGC	TGCCACATTT	GTGGCNTCTN	TTGCACTTGT	480
TTCAAAA						487

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

TGAATTGGCT	AAAAGACTGC	ATTTTTANAA	CTAGCAACTC	TTATTCTTTT	CCTTTAAAAA	60
TACATAGCAT	TAAATCCCAA	ATCCTATTTA	AAGACCTGAC	AGCTTGAGAA	GGTCACTACT	120
GCATTTATAG	GACCTTCTGG	TGGTTCTGCT	GTTACNNTTG	AANTCTGACA	ATCCTTGANA	180
ATCTTTGCAT	GCAGAGGAGG	TAAAAGGTAT	TGGATTTTCA	CAGAGGAANA	ACACAGCGCA	240
GAAATGAAGG	GGCCAGGCTT	ACTGAGCTTG	TCCACTGGAG	GGCTCATGGG	TGGGACATGG	300
AAAAGAAGGC	AGCCTAGGCC	CTGGGGAGCC	CA			332

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

AGGGCGTGGT	GCGGAGGGCG	TTACTGTTTT	GTCTCAGTAA	CAATAAATAC	AAAAAGACTG	60
GTTGTGTTCC	GGCCCCATCC	AACCACGAAG	TTGATTCTC	TTGTGTGCAG	AGTGACTGAT	120
TTTAAAGGAC	ATGGAGCTTG	TCACAATGTC	ACAATGTCAC	AGTGTGAAGG	GCACACTCAC	180
TCCCGCGTGA	TTACATTTA	GCAACCAACA	ATAGCTCATG	AGTCCATACT	TGTAAATACT	240
TTTGGCAGAA	TACTTNTTGA	AACTTGCAGA	TGATAACTAA	GATCCAAGAT	ATTTCCCAAA	300
GTAAATAGAA	GTGGGTGATA	ATATTAATTA	CCTGTTTACA	TCAGCTTCCA	TTTACAAGTC	360
ATGAGCCCAG	ACACTGACAT	CAAACCTAAGC	CCACTTAGAC	TCCTCACCAC	CAGTCTGTCC	420
TGTCATCAGA	CAGGAGGCTG	TCACCTTGAC	CAAATTCTCA	CCAGTCAATC	ATCTATCCAA	480
AAACCATTAC	CTGATCCACT	TCCGTAATG	CACCACCTTG	GTGA		524

(2) INFORMATION FOR SEQ ID NO:209:

120

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGGTGAGGAA ATCCAGAGTT GCCATGGAGA AAATCCAGT GTCAGCATTC TTGCTCCTTG	60
TGGCCCTCTC CTACACTCTG GCCAGAGATA CCACAGTCAA ACCTGGAGCC AAAAAGGACA	120
CAAAGGACTC TCGACCCAAA CTGCCCCAGA CCCTCTCCA	159

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

ACTCCCTGGC AGACAAAGGC AGAGGAGAGA GCTCTGTTAG TTCTGTGTTG TTGAACTGCC	60
ACTGAATTTT TTTCCACTTG GACTATTACA TGCCANTTGA GGGACTAATG GAAAAACGTA	120
TGGGGAGATT TTANCCAATT TANGTNTGTA AATGGGGAGA CTGGGGCAGG CGGGAGAGAT	180
TTGCAGGGTG NAAATGGGAN GGCTGGTTTG TTANATGAAC AGGGACATAG GAGGTAGGCA	240
CCAGGATGCT AAATCA	256

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

ACATTGTTTT TTTGAGATAA AGCATTGAGA GAGCTCTCCT TAACGTGACA CAATGGAAGG	60
ACTGGAACAC ATACCCACAT CTTTGTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT	120
ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTTAAGGAGA	180
GGGGAGATAC ATTCNGAAAG AGGACTGAAA GAAATACTCA AGTNGGAAAA CAGAAAAAGA	240
AAAAAAGGAG CAAATGAGAA GCCT	264

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

121

ACCCAAAAAT	CCAATGCTGA	ATATTTGGCT	TCATTATTCC	CANATTCTTT	GATTGTCAAA	60
GGATTTAATG	TTGTCTCAGC	TTGGGCACTT	CAGTTAGGAC	CTAAGGATGC	CAGCCGGCAG	120
GTTTATATAT	GCAGCAACAA	TATTCAAGCG	CGACAACAGG	TTATTGAACT	TGCCCCGCCAG	180
TTNAATTTCA	TTCCCATTTGA	CTTGGGATCC	TTATCATCAG	CCAGAGAGAT	TGAAAATTTA	240
CCCCTACNAC	TCTTTACTCT	CTGGANAGGG	CCAGTGGTGG	TAGCTATAAG	CTTGGCCACA	300
TTTTTTTTTC	CTTTATTCCT	TTGTCAGA				328

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ACTTATGAGC	AGAGCGACAT	ATCCNAGTGT	AGACTGAATA	AAACTGAATT	CTCTCCAGTT	60
TAAAGCATTG	CTCACTGAAG	GGATAGAAGT	GACTGCCAGG	AGGGAAAGTA	AGCCAAGGCT	120
CATTATGCCA	AAGGANATAT	ACATTTCAAT	TCTCCAAACT	TCTTCCTCAT	TCCAAGAGTT	180
TTCAATATTT	GCATGAACCT	GCTGATAANC	CATGTTAANA	AACAAATATC	TCTCTNACCT	240
TCTCATCGGT						250

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

ACCCAGAATC	CAATGCTGAA	TATTTGGCTT	CATTATTCCC	AGATTCTTTG	ATTGTCAAAG	60
GATTTAATGT	TGTCTCAGCT	TGGGCACTTC	AGTTAGGACC	TAAGGATGCC	AGCCGGCAGG	120
TTTATATATG	CAGCAACAAT	ATTCAAGCGC	GACAACAGGT	TATTGAACTT	GCCCCGCCAGT	180
TGAATTTTCA	TCCCATTTGAC	TTGGGATCCT	TATCATCAGC	CANAGAGATT	GAAAATTTAC	240
CCCTACGACT	CTTTACTCTC	TGGAGAGGGC	CAGTGGTGGT	AGCTATAAGC	TTGGCCACAT	300
TTTTTTTTTC	TTTATTCCTT	TGTCAGAGAT	GCGATTTCATC	CATATGCTAN	AAACCAACAG	360
AGTGACTTTT	ACAAAATTCC	TATAGANATT	GTGAATAAAA	CCTTACCTAT	AGTTGCCATT	420
ACTTTGCTCT	CCCTAATATA	CCTC				444

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

ACTTATGAGC	AGAGCGACAT	ATCCAAGTGT	ANACTGAATA	AAACTGAATT	CTCTCCAGTT	60
TAAAGCATTG	CTCACTGAAG	GGATAGAAGT	GACTGCCAGG	AGGGAAAGTA	AGCCAAGGCT	120

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CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAACT TCTTCCTCAT TCCAAGAGTT	180
TTCAATATTT GCATGAACCT GCTGATAAGC CATGTTGAGA AACAAATATC TCTCTGACCT	240
TCTCATCGGT AAGCAGAGGC TGTAGGCAAC ATGGACCATA GCGAANAAAA AACTTAGTAA	300
TCCAAGCTGT TTTCTACACT GTAACCAGGT TTCCAACCAA GGTGGAATC TCCTATACTT	360
GGTGCC	366

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTGTATAAAC AGAACTCCAC TGCANGAGGG AGGGCCGGGC CAGGAGAATC TCCGCTTGTC	60
CAAGACAGGG GCCTAAGGAG GGTCTCCACA CTGCTNNTAA GGGCTNTNC ATTTTTTTAT	120
TAATAAAAAG TNNAAGGC CTCTTCTCAA CTTTTTCCC TTNGGCTGGA AAATTTAAAA	180
ATCAAAAATT TCTNAAGTT NTCAAGCTAT CATATATACT NTATCCTGAA AAAGCAACAT	240
AATTCTTCCT TCCCTCCTTT	260

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

ACCTACGTGG GTAAGTTTAN AAATGTTATA ATTTTCAGGAA NAGGAACGCA TATAATTGTA	60
TCTTGCTTAT AATTTTCTAT TTTAATAAGG AAATAGCAAA TTGGGGTGGG GGGAATGTAG	120
GGCATTCTAC AGTTTGAGCA AAATGCAATT AAATGTGGAA GGACAGCACT GAAAAATTTT	180
ATGAATAATC TGTATGATTA TATGTCTCTA GAGTAGATT ATAATTAGCC ACTTACCCTA	240
ATATCCTTCA TGCTTGTAAG GT	262

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACCAAGGTGG TGCATTACCG GAANTGGATC AANGACACCA TCGTGGCCAA CCCCTGAGCA	60
CCCCTATCAA CTCCCTTTTG TAGTAACTT GGAACCTTGG AAATGACCAG GCCAAGACTC	120
AGGCCTCCCC AGTTCTACTG ACCTTTGTCC TTANGTNTNA NGTCCAGGGT TGCTAGGAAA	180
ANAAATCAGC AGACACAGGT GTAAA	205

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TACTGTTTTG TCTCAGTAAC AATAAATACA AAAAGACTGG TTGTGTTCCG GCCCCATCCA	60
ACCACGAAGT TGATTCTCT TGTGTGCAGA GTGACTGATT TTAAAGGACA TGGA	114

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

ACTAGCCAGC ACAAAGGCA GGGTAGCCTG AATTGCTTTC TGCTCTTAC ATTTCTTTTA	60
AAATAAGCAT TTAGTGCTCA GTCCTACTG AGT	93

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

ACTANGTGCA GGTGCGCACA AATATTGTC GATATTCCT TCATCTTGGA TTCCATGAGG	60
TCTTTTGCCC AGCCTGTGGC TCTACTGTAG TAAGTTTCTG CTGATGAGGA GCCAGNATGC	120
CCCCACTAC CTTCCCTGAC GCTCCCCANA AATCACCCAA CCTCTGT	167

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

AGGGCGTGGT GCGGAGGGCG GTACTGACCT CATTAGTAGG AGGATGCATT CTGGCACCCC	60
GTCTTTCACC TGTCGCCCAA TCCTTAAAG GCCATACTGC ATAAAGTCAA CAACAGATAA	120
ATGTTTGCTG AATTAAAGGA TGGATGAAAA AAATTAATAA TGAATTTTGG CATAATCCAA	180
TTTTCTCTTT TATATTCTA GAAGAAGTTT CTTTGAGCCT ATTAGATCCC GGGAAATCTTT	240
TAGGTGAGCA TGATTAGAGA GCTTGTAGGT TGCTTTTACA TATATCTGGC ATATTTGAGT	300

CTCGTATCAA AACAAATAGAT TGGTAAAGGT GGTATTATTG TATTGATAAG T

351

(2) INFORMATION FOR SEQ ID NO:223

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAAACAAACA AACAAAAAAA ACAATTCTTC ATTCAGAAAA ATTATCTTAG GGACTGATAT	60
TGGTAATTAT GGTCAATTTA ATWRTRTTKT GGGGCATTTT CTTACATTGT CTTGACAAGA	120
TTAAATGTC TGTGCCAAAA TTTTGTATTT TATTTGGAGA CTTCTTATCA AAAGTAATGC	180
TGCCAAAGGA AGTCTAAGGA ATTAGTAGTG TTCCCMTCAC TTGTTTGGAG TGTGCTATTC	240
TAAAAGATT TGATTTCTCG GAATGACAAT TATATTTTAA CTTTGGTGGG GGAAANAGTT	300
ATAGGACCAC AGTCTTCACT TCTGATACTT GTAAATTAAT CTTTATTGTC ACTTGTTTTC	360
ACCATTAAGC TATATGTTTA AAA	383

(2) INFORMATION FOR SEQ ID NO:224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

CCCCTGAAGG CTTCTTGTTA GAAAATAGTA CAGTTACAAC CAATAGGAAC AACAAAAAGA	60
AAAAGTTTGT GACATTGTAG TAGGGAGTGT GTACCCCTTA CTCCCCATCA AAAAAAAAT	120
GGATACATGG TTAAAGGATA RAAGGGCAAT ATTTATCAT ATGTTCTAAA AGAGAAGGAA	180
GAGAAAATAC TACTTTCTCR AAATGGAAGC CCTTAAAGGT GCTTTGATAC TGAAGGACAC	240
AAATGTGGCC GTCCATCCTC CTTTARAGTT GCATGACTTG GACACGGTAA CTGTTGCAGT	300
TTTARACTCM GCATTGTGAC	320

CLAIMS

1. A polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NOS: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences and variants of said nucleotide sequences.
2. A DNA molecule comprising a nucleotide sequence encoding the polypeptide of claim 1.
3. A DNA molecule having a sequence provided in SEQ ID NOS: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220 and 222-224.
4. An expression vector comprising the DNA molecule of claims 2 or 3.
5. A host cell transformed with the expression vector of claim 4.
6. The host cell of claim 5 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cell lines.
7. A pharmaceutical composition comprising the polypeptide of claim 1 and a physiologically acceptable carrier.
8. A vaccine comprising the polypeptide of claim 1 and a non-specific immune response enhancer.

9. The vaccine of claim 8 wherein the non-specific immune response enhancer is an adjuvant.

10. A vaccine comprising the DNA molecule of claims 2 or 3 and a non-specific immune response enhancer.

11. The vaccine of claim 10 wherein the non-specific immune response enhancer is an adjuvant.

12. A pharmaceutical composition for the treatment of prostate cancer comprising a polypeptide and a physiologically acceptable carrier, the polypeptide comprising an immunogenic portion of a prostate protein or of a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219 and 221, the complements of said nucleotide sequences and variants of said nucleotide sequences.

13. A vaccine for the treatment of prostate cancer comprising a polypeptide and a non-specific immune response enhancer, said polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants of said nucleotide sequences

14. The vaccine of claim 13 wherein the non-specific immune response enhancer is an adjuvant.

15. A vaccine for the treatment of prostate cancer comprising a DNA molecule and a non-specific immune response enhancer, the DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants of said nucleotide sequences.

16. The vaccine of claim 15 wherein the non-specific immune response enhancer is an adjuvant.

17. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the pharmaceutical composition of claims 7 or 12.

18. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the vaccine of any one of claims 8, 10, 13 or 15.

19. A fusion protein comprising two or more polypeptides according to claim 1.

20. A fusion protein comprising a polypeptide according to claim 1 and a known prostate antigen.

21. A pharmaceutical composition comprising a fusion protein according to any one of claims 19-20 and a physiologically acceptable carrier.

22. A vaccine comprising a fusion protein according to any one of claims 19-20 and a non-specific immune response enhancer.

23. The vaccine of claim 22 wherein the non-specific immune response enhancer is an adjuvant.

24. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the pharmaceutical composition of claim 21.

25. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the vaccine of claim 22.



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/12, C07K 14/705, C12N 5/10, 1/21, A61K 38/17, C12N 1/19, A61K 39/00, C12N 15/62	A3	(11) International Publication Number: WO 98/37093 (43) International Publication Date: 27 August 1998 (27.08.98)								
(21) International Application Number: PCT/US98/03492 (22) International Filing Date: 25 February 1998 (25.02.98) (30) Priority Data: <table border="0"> <tr> <td>08/806,099</td> <td>25 February 1997 (25.02.97)</td> <td>US</td> </tr> <tr> <td>08/904,804</td> <td>1 August 1997 (01.08.97)</td> <td>US</td> </tr> <tr> <td>09/020,956</td> <td>9 February 1998 (09.02.98)</td> <td>US</td> </tr> </table> (71) Applicant: CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US). (72) Inventors: XU, Jiangchun; 15805 Southeast 43rd Place, Bellevue, WA 98006 (US). DILLON, Davin, C.; 21607 N.E. 24th Street, Redmond, WA 98053 (US). (74) Agents: MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia Center, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).	08/806,099	25 February 1997 (25.02.97)	US	08/904,804	1 August 1997 (01.08.97)	US	09/020,956	9 February 1998 (09.02.98)	US	(81) Designated States: AL, AM, AT, AU, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims</i> <i>and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 17 December 1998 (17.12.98)
08/806,099	25 February 1997 (25.02.97)	US								
08/904,804	1 August 1997 (01.08.97)	US								
09/020,956	9 February 1998 (09.02.98)	US								
(54) Title: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE (57) Abstract Compounds and methods for treating prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. Vaccines and pharmaceutical compositions for immunotherapy of prostate cancer comprising such polypeptides, or DNA molecules encoding such polypeptides, are also provided, together with DNA molecules for preparing the inventive polypeptides.										

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 98/03492

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C07K14/705 C12N5/10 C12N1/21 A61K38/17
C12N1/19 A61K39/00 C12N15/62

According to International Patent Classification (IPC) or to both national classification and IPO

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C07K C12N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 95 04548 A (JENNER TECHNOLOGIES) 16 February 1995 see the whole document ---	
A	WO 93 25224 A (VETROGEN CORP) 23 December 1993 see the whole document ---	
A	WO 95 30758 A (MAYO FOUNDATION ;HYBRITECH INC (US); TINDALL DONALD J (US); YOUNG) 16 November 1995 see the whole document ---	
A	EP 0 652 014 A (NAT INST IMMUNOLOGY) 10 May 1995 see the whole document ---	
	-/--	

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
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- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *Z* document member of the same patent family

Date of the actual completion of the international search

30 July 1998

Date of mailing of the international search report

03.11.1998

Name and mailing address of the ISA

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Fax: (+31-70) 340-3016

Authorized officer

Oderwald, H

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 98/03492

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>SHORT J M ET AL: "LAMBDA ZAP: A BACTERIOPHAGE LAMBDA EXPRESSION VECTOR WITH IN VIVO EXCISION PROPERTIES" NUCLEIC ACIDS RESEARCH, vol. 16, no. 15, 1988, pages 7583-7600, XP002007597 see the whole document & "AC No. AA453562" EMBL SEQUENCE DATABASE, 10 May 1990, HEIDELBERG, GERMANY, see nucleotides 398-765 ---</p>	2,4-6
X,P	<p>HILLIER L ET AL: "Homo sapiens cDNA clone 788180 (AC No. AA453562)" EMBL SEQUENCE DATABASE, 11 June 1997, HEIDELBERG, GERMANY, XP002073072 see the whole document -----</p>	2,4-6

INTERNATIONAL SEARCH REPORT

Ir. ational application No.

PCT/US 98/03492

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claims 17, 18, 24 and 25 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see further information sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

see further information sheet, subject 1.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-11 and 17-25 all partially

A polypeptide comprising an immunogenic portion or a variant of a prostate protein encoded by SEQ ID NO:2, DNA molecules related to said protein, expression vectors comprising said DNA molecules, hosts transformed with said vectors, fusion proteins comprising said polypeptide, pharmaceutical compositions and vaccines comprising said polypeptide, fusion proteins and DNA.

2. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 3.

3. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 8.

4. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 9.

5. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 10.

6. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 11.

7. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 12.

8. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 13.

9. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 14.

10. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 15.

11. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 16.

12. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 17.

13. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 18.

14. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 19.

15. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 20.

16. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 21.

17. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 22.

18. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 23.

19. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 24.

20. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 25.

21. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 26.

22. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 27.

23. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 28.

24. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 29.

25. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 41.

26. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 42.

27. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 43.

28. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 44.

29. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 45.

30. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 47.

31. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 48.

32. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210.

same as invention 1 but for SEQ ID NO: 49.

33. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 50.

34. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 51.

35. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 52.

36. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 54.

37. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 55.

38. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 56.

39. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 57.

40. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 58.

41. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 59.

42. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 60.

43. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 61.

44. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 62.

45. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 63.

46. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 64.

47. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 65.

48. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 70.

49. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 73.

50. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 74.

51. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 79.

52. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 81.

53. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 87.

54. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 90.

55. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 92.

56. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 93.

57. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 97.

58. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 103.

59. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 104.

60. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 107.

61. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 109.

62. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 110.

63. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 111.

64. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 115.

65. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 116.

66. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 117.

67. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 118.

68. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 119.

69. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 120.

70. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 121.

71. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 122.

72. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 123.

73. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 124.

74. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 125.

75. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 126.

76. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 127.

77. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 128.

78. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 129.

79. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 130.

80. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 131.

81. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 132.

82. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 133.

83. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 134.

84. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 135.

85. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 136.

86. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 137.

87. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 138.

88. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 139.

89. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 140.

90. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 141.

91. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 142.

92. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 143.

93. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 144.

94. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 145.

95. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 146.

96. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 147.

97. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 148.

98. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 149.

99. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 150.

100. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 151.

101. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 152

102. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 153.

103. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 154.

104. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 155.

105. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 156.

106. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 157.

107. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 158.

108. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 159.

109. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 160.

110. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 171.

111. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 173.

112. Claims: 1-11 and 17-25

same as invention 1 but for SEQ ID NO: 174.

113. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 175.

114. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 177.

115. Claims: 1-11 and 17-25

same as invention 1 but for SEQ ID NO: 181.

116. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 188.

117. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 191.

118. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 193.

119. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 194.

120. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 198.

121. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 203.

122. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 204.

123. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 207.

124. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 209.

125. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 210.

126. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 211.

127. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 220.

128. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 222.

129. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 223.

130. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 224.

131. Claims: 12-18 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Pharmaceutical compositions and a vaccines comprising an immunogenic portion or a variant of a prostate-specific polypeptide and related DNA sequences, said DNA sequences recited in SEQ ID NO: 5.

132. Claims: 12-18 all partially

same as invention 131 but for SEQ ID NO: 6.

133. Claims: 12-18 all partially

same as invention 131 but for SEQ ID NO: 7.

134. Claims: 12-18 all partially

same as invention 131 but for SEQ ID NO: 30.

135. Claims: 12-18 all partially

same as invention 131 but for SEQ ID NO: 31.

136. Claims: 12-18 all partially

same as invention 131 but for SEQ ID NO: 32.

137. Claims: 12-18 all partially

same as invention 131 but for SEQ ID NO: 33.

138. Claims: 12-18 all partially

same as invention 131 but for SEQ ID NO: 34.

139. Claims: 12-18 all partially

same as invention 131 but for SEQ ID NO: 35.

140. Claims: 12-18 all partially

same as invention 131 but for SEQ ID NO: 36.

141. Claims: 12-18 all partially

same as invention 131 but for SEQ ID NO: 37.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

142. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 38.
143. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 39.
144. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 40.
145. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 46.
146. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 53.
147. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 66.
148. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 67.
149. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 68.
150. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 69.
151. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 71.
152. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 72.

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153. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 75.
154. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 76.
155. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 77.
156. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 78.
157. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 80.
158. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 82.
159. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 83.
160. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 84.
161. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 85.
162. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 86.
163. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 88.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

164. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 89.
165. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 91.
166. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 94.
167. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 95.
168. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 96.
169. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 98.
170. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 99.
171. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 100.
172. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 101.
173. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 102.
174. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 105.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

175. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 106.
176. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 161.
177. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 162.
178. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 163.
179. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 164.
180. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 165.
181. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 166.
182. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 167.
183. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 168.
184. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 169.
185. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 170.

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186. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 179.
187. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 180.
188. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 182.
189. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 183.
190. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 184.
191. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 185.
192. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 186.
193. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 187.
194. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 189.
195. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 190.
196. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 192.

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197. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 195.
198. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 196.
199. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 197.
200. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 199.
201. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 200.
202. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 201.
203. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 202.
204. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 205.
205. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 206.
206. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 208.
207. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 212.

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208. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 213.
209. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 214.
210. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 215.
211. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 216.
212. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 217.
213. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 218.
214. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 219.
215. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 221.

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